AppendixA

01:53 2003

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

November 21, 2003, 13:35:18 ; Search time 18 Seconds (without alignments) 608.735 Million cell updates/sec Run on:

US-09-972-970-4
1283
1 MPGKHQHFQEPEVGCCGKYF.....RAPYTPKAVWASLRSGCRTT 233 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Searched:

127863 segs, 47026705 residues

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	O60628 homo sapien		mus	\sim	ratti	homo	homo ?	11 mus 1	mus	Q9mym2 cercopithec		O75954 homo sapien	Q62283 mus musculu	P19397 homo sapien	homo	rattı	homo	P27701 homo sapien	1 mus n	P40237 mus musculu	Q9xsk2 bos taurus	ratt	Q8wmq3 sus scrofa	٥,	Q28709 oryctolagus	m	P35762 mus musculu	P40240 mus musculu	5 ratt	Q9n0j9 saquinus oe	'n	18582	P40241 rattus norv
SUMMARIES		ID	T4S9 HUMAN	TNE7 HUMAN	T4S7 MOUSE	T4S7 HUMAN	C151_RAT	T4S6_HUMAN	T4S2 HUMAN	T4S6_MOUSE	CD53_MOUSE	C151_CERAE				CD53_HUMAN				CD82_HUMAN	CD63_MOUSE	CD82_MOUSE	CD63_BOVIN	CD82 RAT	CD9_PIG	CD63 HUMAN	CD63_RABIT		CD81_MOUSE	5	- 1	CD81_SAGOE	CD81_CERAE	CD81 HUMAN	CD9_RAT
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		Length	268	294	238	238	253	245	249	245	218	253	253	239	249	219	253	218	237	267	237	266	236	266	225	237	237	237	236	225	236	236	236	236	225
d	Query	Match		25.3	•	18.9	•	٠	18.7	18.7			٠	•	٠.	٠.			٠.	•	17.1			16.8			٠,		Ġ.	ė.	ė.			16.1	
		Score	æ	324	EO.	マ	24	•		239.5	239	239	239	236		235.5		233.5	231	228	220	217	215.5	215.5	214.5	214	214 223	211	210	208	208	208	207	207	506
	Result	No.	1	7	m	4	S	9	7	ω (σ.	10	11	12	13	14	15	16	. 17	18	13	20	21	. 22	23	4. 1	67	26	. 27	28	29	30	31	35	23

P30409 cercopithec P21926 homo sapien Q61470 mus musculu P31053 rattus norv P40239 felis silve Q922j6 mus musculu Q9jiwi rattus norv P19331 schistosoma Q26499 schistosoma P30932 bos taurus P57591 schistosoma P30932 bos taurus P60536 homo parion P60536 homo	משלמה סייסיו סריססס
CD9 CERAE CD9—HUMAN CD37—MOUSE CD37—RAT CD9—FELCA TSN2—MOUSE TSN2—RAT TSN2—RAT TN23—SCHPA IN23—SCHPA IN23—SCHPA CD9—BOVIN IN23—SCHPA CN2—HUMAN	
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227 2281 2281 225 221 221 2218 2218 225 225	1
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202 201 200.5 200.5 199 197 195.5 190.5 188	
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ALIGNMENTS

Mon Nov 24 10:01:53 2003

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RA Attausberg R.L. Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Strausberg R.L., Feingold E.A., Grouse L.H., Schaefer C.F., Bhat N.K., Klausner R.D., Colling F.S., Wagner L., Schaefer C.F., Bhat N.K., Rausner R.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hong L., Robins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L., Bratchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Bratchenko L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Rapseleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C., R. Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C., R.A. Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C., R. Brownstein M.J., Vadin T.B., Toshiyuki S., Malek J.J., Hulyk S.W., RA Richards S., Worley K.C., Hale S., Garigues R.D., Hulyk S.W., Sodergren E.J., Lu X., Gibbs R.A., Hulyk S.W., Sodergren E.J., Lu X., Gibbs R.A., Halting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Rakeley R.W., Touchman J.W., Schmutz J., Myers R.M., Rakeley R.W., Touchman J.W., Schmutz J., Myers R.M., Scheil J. S.N., Marra M.A., Scheil J. S., Jones S.J.M., Marra M.A., Scheil J. S., Jones S.J.M., Marra M.A., F., Wennerch A., Scheil J. S., Jones S.J.M., Marra M.A., F., Wennerch A., Scheil J. S., Jones S.J.M., Marra M.A., F., Wennerch A., Scheil J. S., Jones S.J.M., Marra M.A., F., Wennerch A., Scheil J. S., Jones S.J.M., Marra M.A., F., Wennerch A., Scheil J. J., Jones S.J.M., Marra M.A., F., Wennerch A., Scheil J. J., Jones S.J.M., Marra M.A., F., Wennerch A., Scheil J. J., Jones S.J.M., Marra M.A., F., Wennerch A., Scheil J. J., Jones S.J.M., Marra M.A., F., Wennerch A., Scheil J. J., Jones S.J.M., Marra M.A., F., Wennerch A., Scheil J. J., Jones S.J.M., Marra M.A., F., Wennerch A., Scheil J. Jones S.J.M., Marra M.A., M.A., Jones S.J.M., Marra M.A., Mell J. Jones S.J.M., Marra M.A., Jones S.J.M., Ma POTENIAM: (POTENTIAL)

"TYOPLASMIC (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
"-TANYED (GLCNAC. . .) (POTENTIAL) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. POTENTIAL. EXTRACELLULAR (POTENTIAL). 71A6DC64D6CA6BAE CRC64; EXTRACELLULAR (POTENTIAL) CYTOPLASMIC (POTENTIAL). CYTOPLASMIC (POTENTIAL) SEQUENCE FROM N.A. V., Dessen P., Boucheix C.; Rubinstein B., Serru V., Dessen P., Boucheix C.; "New tetrapase."; "New tetrapas identified in the EST databases."; gubmitted (JAN-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF120266; AAD17295.1; -EMBL; BC004157; AAH04161.1; -EMBL; BC004161; AAH04461.1; -EMBL; BC008161; Cintegral to plasma membrane; TAS.
GO; GO:0005897; C:integral to plasma membrane; TAS. N-LINKED POTENTIAL Pfam; PF00335; transmembrane4; 1. Pfam; PF051E; PS00421; TM4 1; FALSE_NEG-Glycoprotein; Transmembrane. InterPro; IPR000301; Transmem_4. 33165 MW; Query Match Best Local Similarity 33.9% warrhes 64; Conservative 44 62 83 93 114 189 230 294 AA; SEQUENCE FROM N.A. Glycoprotein; NCBI_TaxID=9606; CARBOHYD CARBOHYD SEQUENCE DOMAIN TRANSMEM DOMAIN TRANSMEM RANSMEM TRANSMEM CARBOHYD DOMAIN DOMAIN

18 KYFLFGFNIVFWVLGALFLAIGLWAWGEKGVLSNISALTDLGGLDPVWLFVVVGGVMSVL

8

095858; 16-007-2001 (Rel. 40, Last sequence update) 6-007-2001 (Rel. 40, Last sequence update) 15-5EP-2003 (Rel. 42, Last annotation update)

etraspan NET-7

STANDARD;

RESULT 2 TNE7 HUMAN ID TNE7 HUMAN

3,

Gaps

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OM protein - protein search, using sw model

November 21, 2003, 13:35:18; Search time 18 Seconds (without alignments) 608.735 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-972-970-4 1283 1 MPGKHQHPQEPEVGCCGKYF.....RAPYTPKAVWASLRSGCRTT 233

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 segs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	O60628 homo ganien	9 homo	m snm		rattu	043657 homo sapien	homo	O70401 mus musculu	Q61451 mus musculu	cerc		075954 homo sapien	m snm	homo	homod	rattu	homo sa	рошо	m snm 1	mus	Q9xsk2 bos taurus	ratt	Q8wmg3 sus scrofa	P08962 homo sapien	oryct		ď	P40240 mus musculu	5 ratt	6	_	~	1 rattu
SUMMARIES	ID	T4S9 HUMAN	TNE7 HUMAN	T4S7 MOUSE	T4S7_HUMAN	C151_RAT	T4S6_HUMAN	T4S2_HUMAN	T4S6_MOUSE	CD53_MOUSE	C151_CERAE	C151_MOUSE	TNES_HUMAN	T4S2_MOUSE	CD53 HUMAN	C151_HUMAN	CD53_RAT	T4S3 HUMAN	CD82_HUMAN	CD63_MOUSE		CD63_BOVIN		CD9_PIG	CD63_HUMAN	CD63_RABIT		CD81_MOUSE				⊣'		CD9_RAT
	DB	-			•		•	7	•	Н	7	-	п	7	~1	н	-	-	H	Н	-	-	7	~	-		7				7	Н	Н	-
	Length	268	294	238	238	253	245	249	245	218	253	253	239	249	219	253	218	237	267	237	266	236	266	225	237	237	237	236	225	236	236	236	236	225
de	Query Match	69.0	'n			•	ω.	•		٠	18.6	٠	٠.	•		٠	٠	•	17.8		16.9	16.8	•	•	16.7	16.7	•	16.4		16.2	16.2		16.1	16.1
	Score	885	324	251	243		240.5		239.5	239	239	239	236		235.5		233.5	231	228	220		215.5	215.5	214.5	214	214	211	210	208	208	208	207	207	206
	Result No.	-	7	m	4	v	9	7	σο .	ח	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	52	56	27	28	59	30	31	32	33

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cerco											homo sapien	
P30409	P21926	061470	P31053	P40239	Q922j6	1w1	P19331	Q26499	P30932	P27591	969090	
CD9_CERAE	CD9 HUMAN	CD37_MOUSE	CD37_RAT	CD9_FELCA	TSN2_MOUSE	TSN2_RAT	IM23_SCHMA	IM23_SCHHA	CD9 BOVIN	IM23 SCHJA	TSN2_HUMAN	
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227	22.7	281	281	225	221	221	218	218	225	218	221	
15.7	15.7	15.6	15.6	15.5	15.4	15.4	15.2	14.8	14.7	14.7	14.7	
202	201	200.5	200.5	199	197	197	195.5	190.5	189	188.5	188	
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ALIGNMENTS

RESULT 1

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sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 LDPVWLFVVVGGVMSVLGFAGCIGALRENTFLLKFFSVFLGLIFFLELATGILAFVFKDW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IRDQLNFFINNNVKAYRDDIDLQNLIDFAQEYWSCCGARGPNDWNLNIYFNCTDLNPSRE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A59261; A59261.

MGD; MGI:1928096; Tm48f9.

MGD; GO:0016021; C:integral to membrane; TAS.

GO; GO:0016021; C:integral to membrane; TAS.

InterPro; IPR00301; Transmem1 4.

Prim; PR00359; Transmembrane4; 1.

PRINTS; PR00359; TMFOUR;

PR00315; TMFOUR 1; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MPGKHQHFQEPEVGCCCKYFLFGFNIVFWVLGALFLAIGLWAMGEKGVLSNISALTDLGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MSGK--HYKGPEVSCCIKYFIFGFNVIFWFLGITFLGIGLWAWNEKGVLSNISSITDLGG 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Gaps
                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
MISSING (IN REP. 1).
Garcia-Frigola C., de Lecea L., Soriano E.;
"Mouse Tspan-5 cDNA cloning.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
-!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          tch 69.0%; Score 885; DB 1; Length 268; al Similarity 79.9%; Pred. No. 1.4e-67; 155; Conservative 16; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL).
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16-0CT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
NET7.
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                                                                                                                                              EMBL, AF053455, AAC69712.1; --
EMBL, AF065389; AAC17120.1; --
EMBL, BC009704; AAH09704.1; --
EMBL, AF121344; AAF28869.1; --
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268 AA;
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ID TNET HUM

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DT 16-0CT-2

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                                                                                                                                                                                                                                                                                                                                                                                                      WEDLINE-Kidney;

X. TISSUB-Kidney;

X. Actausherg Rich, Feingold E.A., Gruuse L.H., Derge J.G.,

X. Stausherg R.D., Feingold E.A., Gruuse L.H., Schaefer C.M., Schuler G.D.,

X. Altausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

X. Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

X. Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

X. Altachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

X. Altachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

X. Altachenko L., Marusina K., Farmer A.A., Rubin G.M., Scheetz T.E.,

R. Archards S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

R.A. Robers S.S., Morley K.C., Hale S., Garcia A.M., Gaburatne P.H.,

R. Richards S., Worley K.C., Hale S., Garcia A.M., Gaburatne P.H.,

R. Ayilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

W. Halton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

R. Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

R.A. Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

R. Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

R. Generation and initial analysis of more than 15,000 full-length

R. Proc. Natl. Acad. Sci. U.S.A., 99:169013(2002).

C. I. SUBCELLULAR LOCATION: Integral membrane protein (Probable).

C. I. SUBCELLULAR F. Belongs to the tetraspanin (TM4SF) family.
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Best Local Similarity 33.9%; Pred. No. 2.6e-20;
Matches 64; Conservative 45; Mismatches 70; Indels 10; Gaps
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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N-LINKED (GLCNAC. . ) (POTENTIAL)
N-LINKED (GLCNAC. . ) (POTENTIAL)
                                                                                                                                                                        SEQUENCE FROM N.A. Rubinstein B., Boucheix C.; Rubinstein B., Serru V., Dessen P., Boucheix C.; Now tetraspans identified in the EST database."; Submitted (ANN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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EMBL, BC003157, AAH03157.1; -.
EMBL, BC00161, AAH03167.1; -.
EMBL, BC0005897, C:integral to plasma membrane; TAS.
GO; GO:0005824; C:membrane fraction; TAS.
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PROSITE; PS00421; TM4_1; FALSE_NEG.
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DOMAIN
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18 KYFLFGFNIVFWVLGALFLAIGLWAWGEKGVLSNISALTDLGGLDPVWLFVVVGGVMSVL 77

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SEQUENCE TISSUE-Kidney;

M. Marada A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Azawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Azawa K., Tawam M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Azawa K., Tawam M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Azawa K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

A Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

A Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

A Ruehl P., Lewis S., Matsudo I., Gissi C., King B., Kochiwa H.,

Kuehl P., Lewis S., Matsudo I., Gissi C., King B., Kochiwa H.,

A Schriml L.M., Staubli F., Suruki R., Tomita M., Wagner L., Washio T.,

B Bake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

B Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

B Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

B Brownstein M.J., Bult C., Riecher C., Fujita M., Saroch K.-F.

A Sasaki H., Saro K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.

Sazuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Nordone P., Kohtsuki S.,
                                                     MEDLINE=22388257; PubMed=12477932;
A Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
A Altausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altachul S.F., Zeeberg B., Buercow K.H., Schaefer C.F., Bhat N.K.,
A Altachul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Aplatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Rapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
A Rapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Perers G.J., Abramson R.D., Mullahy S.J.,
A Raha S.A., McEwan P.J., McKerran K.J., Malek J.A., Gunaratne P.H.,
A Nillalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
A Hating M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Bakesley R.W., Touchman J.W., Schen E.D., Dickson M.C.,
A Batkesley R.W., Touchman J.W., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
A Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length
                                   GFAGCIGALRENTFLLKFFSVFLGLIFFLELATGILAFVFKDWIRDQLNFFINNNVKAYR 137
21 KFSLIIYSTVFWLIGALVLSVGIYAEVERQKYKTLES----AFLAPAIILILLGVVMFMV 76
                                                                                                                           DDIDLONLIDFAQEYWSCCGARGPNDWNLNIYFNCTDLNPSRERCGVPFSCCVRDPAMSS
                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                     (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                        238 AA
                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane 4 superfamily, member 7.
                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                             191 TEVVNTMCG 199
                                                                                                                                                                             TPSVAMMSG 206
                                                                                                                                                                                                                                                                                                                                                                                                                              musculus (Mouse).
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T4S7_M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72 GVMSVLGFAGCIGALRENTFLLKFFSVFLGLIFFLELATGILAFVFKDWIRDQLNFFINN 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 TFVMAIGFVGCIGALKENKCLLLTFFVLLLVFLLEATIAVLFFAYSDKIDSYAQQDLKK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 GLHLYGTQGNVGLTNAMSIIQTDFRCCGVSNYTDW-FEVY-----NATR----VPDSCC 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 GCLQGVKYLMFAFNLLFWLGGCGVLGVGIWLAATQGNFATLS--SSFPSLSAANLLIVTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  132 NVKAY -- RDDIDLONLIDFAQEYWSCCGARGPNDWNLNIYFNCTDLNPSRERCGVPFSCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 GCCG--KYFLFGFNIVFWVLGALFLAIGLWAWGEKGVLSNISALTDLGGLDPVWLFVVVG
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EXTRACELLULAR (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24;
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15-JUL-1998 (Rel. 36, Last sequence update)
15-SPC-2003 (Rel. 42, Last annotation update)
Transmembrane 4 superially, member 7 (Novel antigen 2) (NAG-2)
(Tetraspanin 4) (Tspara1).
        19.6%; Score 251; DB 1; Length 238; 31.3%; Pred. No. 3e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
EXTRACELLULAR (POTENTIAL).
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human and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                  MGD; MGI:1928097; Tm4sf7.
InterPro; IPR000301; Transmem 4.
Pfam; PF00335; transmembrane4; 1.
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MEDLINE=98030601; PubMed=9360996;
                                                                                                                                                                                                                                                                             EMBL; AK002709; BAB22301.1; -. EMBL; BC003482; AAH03482.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26053 MW;
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PROSITE; PS00421; TM4 1; 1.
Glycoprotein; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TM4SF7 OR NAG2 OR TSPAN4.
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76
85
106
201
222
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152
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238 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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014817;
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Tachibana I., Bodorova J., Berditchevski F., Zutter M.M., Hemler M.E.; "NAG-2, a novel transmembrane-4 superfamily (TM4SF) protein that complexes with integrins and other TM4SF proteins."; J. Biol. Chem. 272:29181-29189(1997).
                                                               MEDLINE=98390278; PubMed=9714763; Todd S.C., Doctor V.S., Levy S.; "Sequences and expression of six new members of the tetraspanin/TM4SF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                                                                               family.",
Biochim. Biophys. Acta 1399:101-104(1998)
                                                                                                                                                  MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF022813; AAC51864.1; -. EMBL; AF054841; AAC69717.1; -.
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PROSITE; PS00421; TM4 1; 1.
Glycoprotein; Transembrane.
DOMAIN
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Genew; HGNC:11859; TM4SF7.
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34
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76
106
221
222
222
238
                                                     SEQUENCE FROM N.A.
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                                                                                                                                         TISSUE=Lung
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TRANSMEM
DOMAIN
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                 GFAGCIGALRENTFLLKFFSVFLGLIFFLELATGILAFVFKDWIRDQLNFFINNNVKAY- 136
                                                                                                                                                                                                                                                                                                                                                                                      68 GFVGCLGAIKENKCLLLFFLLLLLVFLLEATIAILFFAYTDKIDRYAQQDLKKGLHLYG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            137 -RDDIDLQNLIDFAQEYWSCCGARGPNDWNLNIYFNCTDLNPSRERCGVPFSCCVRDPAM 195
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                                                                                                                                                                                                                                                           10 KYLMFAFNLLFWLGGCGVLGVGWLAATQGSFATLS--SSFPSLSAANLLITGAFVMAI 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hua L.V., Green M., Wong A., Warsh J.J., Li P.P.;
"Tetraspan protein CD151: a common target of mood stabilizing drugs?";
Neuropsychopharmacology 25:729-736 (2001).
-! SUBCELLULAR LOCATION: Integral membrane protein.
-! SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
                                                                                                                                                                                                                          18 KYFLFGFNIVFWVLGALFLAIGLWAWGEKGVLSNISALTDLGGLDPVWLFVVVGGVMSVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rođentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                           Gaps
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CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                           Indels 24;
   .) (POTENTIAL)
                                                                                            Query Match
18.9%; Score 243; DB 1; Length 238;
Best Local Similarity 29.7%; Pred. No. 1.4e-13;
Matches 62; Conservative 33; Mismatches 90; Indels
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16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Platelet endothelial tetraspan antigen 3 (CD151 antigen)
CD151 OR PETA3.
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POTENTIAL.
CYTOPLASMIC (POTENTIAL).
POTENTIAL.
EXTRACELULAR (POTENTIAL).
POTENTIAL.
161 161 N-LINKED (GLCNAC. . .) (PC
238 AA; 26118 MW; A6B9A5633065A492 CRC64;
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51876AF31B4DCB2B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    253 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          196 SSTPSVAMMSGSNWSWSSRAP-YTPKAVW 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     172 EFSESCGLHAPGTW-W--KAPCYETVKVW 197
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28355 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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CARBOHYD
SEQUENCE
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                                                                                      WLFVVVGGVMSVLGFAGCIGALRENTFLLKFFSVFLGLIFFLELATGILAFVFKDWIRDQ 124
                                                                                                                                                LNFFINNN-----VKAYRDD--IDLQNLIDFAQEYWSCCGARGPNDWNLNIYFNCTDLNP 177
                                                                    61
                                            FOEPEVGC----CGKYFLFGFNIVFWVLGALFLAIGLWAWGEKGVLSNISALTDLGGLDPV 64
                                                        62 YILVVAGVVWYTGVLGCCATFKERRNLLRLYFILLLIIFLLEIIAGILAYVY----YQQ
                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Transmembrane 4 superfamily, member 6 (Tetraspanin 6) (Tspan-6) (T245
protein) (Tetraspanin TM4-D) (Al5 homolog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Maeda K., Matsuhashi S., Hori K., Xin Z., Mukai T., Tabuchi K., Egashira M., Niikawa N.; "Cloning and characterization of a novel human gene, TM4SF6, encoding a protein belonging to the transmembrane 4 superfamily, and mapped to
                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98390278; Pubmed=9714763; Todd S.C., Doctor V.S., Levy S.; "Sequences and expression of six new members of the tetraspanin/TM4SF
                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Ovary,
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Maeda K., Matsuhashi Y.;
Maeda K., Matsuhashi Y.;
"The CDNA cloning of a novel gene A15 homologue which encords a member of the transmembrane 4 superfamily.";
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                      20;
  Length 253;
Query Match
18.9%; Score 242; DB 1; Length 25;
Best Local Similarity 32.3%; Pred. No. 1.8e-13;
Matches 62; Conservative 28; Mismatches 82; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Puls K.L., Ni J., Liu D., Morahan G., Wright M.D., "The molecular characterization of four tetraspanins.", Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                            245 AA
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                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=99000849; PubMed=9782095;
                                                                                                                                                                               SRERCGVPFSCC 189
                                                                                                                                                                                                   SRV---VPDSCC 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kq22.";
Genomics 52:240-242(1998)
                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (SEP-1999)
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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043657;
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Hopkine R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Robak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length

"Thuman and mouse CDN, sequences.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 LDPVWLFVVVGGVMSVLGFAGCIGALRENTFLLKRFSVFLGLIFFLELATGILAFVFKDW 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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POTENTIAL.
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POTENTIAL.
EXTRACELLULAR (POTENTIAL)
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A -> T (IN dbSNP:1802288)
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811FAB19C2805BE2 CRC64;
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CYTOPLASMIC (POTENTIAL).
POTENTIAL.
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llarity 31.6%; Pred. No. 2.3e-13;
Conservative 30; Mismatches 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000301; Transmem 4.
Pfam; PF00035; transmembrane4; 1.
PRINTS; PR00259; TMF0UR.
PR051TE; PS00421; TM4 1; 1.
Transmembrane; Glycoprotein; Poly
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EMBL; AF043906; AAC64257.1; -.
EMBL; U84895; AAD00560.1; -.
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Best Local Similarity
Matches 61; Conserv
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177 PSRERCGVPFSCC 189

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TISSUE=Brain;

X MEDINE=22388257; PubMed=12477932;

X Klausher R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,

X Klausher R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,

R Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hasheh F.,

Blatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

R Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

R Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

R Rohnstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Mullahy S.J.,

R Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

R Richards S.W., Worley R.M., Sodergren E.J., Lu X., Gibbs R.A.,

R Halton D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

R Halton D.K., Munny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

R Halton B., Madna A., Young A.C., Shevchenko Y., Bouffard G.G.,

R Halteeley R.W., Madna J.W., Schmutz J., Myers R.M.,

R Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
                                                                                                                                                                                                                                                 P417<u>7</u>2; QBWVGS; Q9UEY9;
01-NOV-1995 (Rel. 3), Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Transmembrane 4 superfamily, member 2 (Cell surface glycoprotein Al5)
(T-cell acute lymphoblastic leukemia associated antigen 1) (TALLA-1)
(Membrane component, X chromosome, surface marker 1) (CD231 antigen).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Takagi S., Fujikawa K., Imai T., Fukuhara N., Fukudome K., Minegishi M., Tsuchiya S., Konno T., Hinuma Y., Yoshie O.; "Identification of a highly specific surface marker of T-cell acute lymphoblastic leukemia and neuroblastoma as a new member of the Lransmembrane 4 superfamily."; Int. J. Cancer 61:706-715(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND VARIANT XMLR HIS-172.

MEDLINE-2012017; PubMed=10655063;

Zemni R., Bienvenu T., Vinet M.C., Sefiani A., Carrie A., Billuart McDonell N., Couvert P., Francis F., Chafey P., Fauchereau F., Friocourt G., desportes V., Cardona A., Frints S., Meindl A., Brandau O., Ronce N., Moraine C., Bokhoven H.V., Ropers H.-H., Sudbrak R., Kahn A., Fryns J.-P., Beldjord C., Chelly J.;

"A new gene involved in X-linked mental retardation identified by Mat. Genet. 24:167-170(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE=Peripheral blood lymphocytes;
MEDLINE=93131291; PubMed=8420826;
Emi N., Kiacori K., Seto M., Ueda R., Saito H., Takahashi T.;
"Isolation of a novel cDNA clone showing marked similarity to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wang H., Gao X., Huang Y., Han J.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                       249 AA
                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 4-249 FROM N.A.
TISSUE=Peripheral blood;
MEDLINE=95286314; Pubmed=7768645;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ME491/CD63 superfamily.";
Immunogenetics 37:193-198(1993)
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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                                                                                                                                                                                HUMAN
T4S2 HUMAN
                                      셤
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatic and the Embl. outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGKYFLFGFNIVFWVLGALFLAIGLWAWGEKGVLSNISALTDLGGLDPVWLFVVVGGVMS 75
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences."

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-!- SUBCELLUIAR LOCATION: Integral membrane protein.

-!- TISSUB SPECTRICITY: NOT SOLELY EXPRESSED IN T CELLS. EXPRESSED IN
ACUTE MYELOCYTIC LEUKENIA CELLS. OF SOME PATIENTS.

-!- DISEASE: Defects in TM4SF2 are the cause of a form of X-linked
non-specific mental retardation (XLMR).

-!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.

-!- DATABASE: NAME=PROW, NOTE=PROW 1:38-40 (2000);

WWW#"http://www.ncbi.nlm.nlh.gov/prow/guide/501790534_g.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81, Indels 12; Gaps
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(YTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
P -> H (IN MRX).
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CYTOPLASMIC (POTENTIAL).
POTENTIAL.
EXTRACELLULAR (POTENTIAL).
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POTENTIAL.
EXTRACELLULAR (POTENTIAL)
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E -> K (IN REF. 5).
A -> T (IN REF. 5).
E -> K (IN REF. 3).
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Local Similarity 28.2%; Pred. No. 2.6e-13;
hes 50; Conservative 34; Mismatches 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO:0005887; C:integral to plasma membrane;
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30; GO:0009405; P:pathogenesis; TAS.
InterPro; IPR000301; Transmem 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D10653; BAA01501.1; ALT_INIT.
EMBL; AJ250562; CAB65594.1;
EMBL; AJ250563; CAB65594.1; JOINED.
EMBL; AJ250564; CAB65594.1; JOINED.
EMBL; AJ250564; CAB65594.1; JOINED.
EMBL; AJ250566; CAB65594.1; JOINED.
EMBL; AJ250566; CAB65594.1; JOINED.
EMBL; AJ250566; CAB65594.1; JOINED.
EMBL; AJ250567; CAB65594.1; JOINED.
EMBL; AJ250567; CAB65594.1; JOINED.
EMBL; AB062057; BAB55824.1; GENEL; BAD62057; BAB55824.1; GENEL; BC18036; AM18036.1; GENEL; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00335; transmembrane4; 1
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PROSITE, PS00421; TM4 1; 1.
Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53
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249 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 IKNSFKSNYENALKEYNSTGDYRSEAVDKIQSTLHCCGVTNYGDWKGTNYYSET----
                                                                                                                                                                                                                                                                                                                                                                                                    "Gene structure, chromosomal localization, and protein sequence of mouse CD53 (Cd53): evidence that the transmembrane 4 superfamily arose by gene duplication.", Int. Immunol. 5:209-216(1993).
                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi; Muridae, Murinae, Mus
                                                                                                                                       CD53_MOUSE STANDARD; PRT; 218 AA.
061451; 061721;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Leukocyte surface antigen CD53 (Cell surface glycoprotein CD53)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40;
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N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 18.6%; Score 239; DB 1; Length 218; 1 Similarity 30.9%; Pred. No. 2.8e-13; 63; Conservative 29; Mismatches 72; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
                                                                                                                                                                                                                                                                                                                                                                         Wright M.D., Rochelle J.M., Tomlinson M.G., Seldin M.F., Williams A.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BCAS92EADCE15E3D CRC64;
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Glycoprotein; Antigen; Transmembrane
                                                                                                                                                                                                                                                                                                                                            STRAIN=129/Sv;
MEDLINE=93200067; PubMed=8452817;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:88341; CdS3.
InterPro; PPR003031; Transmem 4.
Pfan; PF00335; transmembrane4; 1.
PRINTS; PR00259; TMFOUR.
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                                 180 ERCGVPFSCC 189
                                                               172 --- GFPKSCC 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              218 AA;
                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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1 VFGLFGCFATCRGSPWMLKLYAMFLSLVFLAELVAGISGFVFRHEIKDTFLRTYTDAMQT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 LDPVWLFVVVGGVMSVLGFAGCIGALRENTFLLKFFSVFLGLIFFLELATGILAFVPKDW 120
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                                            136 YRDDIDLQNLIDFAQEYWSCCGARGPNDWNLNIYFNCTDLNPSRERCGVPFSCCVRD 192
                                                                              ----LEHGIPPSCCMNE 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MPGKHOHFOEPEVGCCGKYFLFGFNIVFWVLGALFLAIGLWAWGEKGVLSNISALTDLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDINE-99190278; PubMed=9714763; Todd S.C., Doctor V.S., Levy S.; "Sequences and expression of six new members of the tetraspanin/TM4SF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                               16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Transmembrane 4 superfamily, member 6 (Tetraspanin 6) (Tspan-6).
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                                                                                                                                                                                                                                                                                                                                                                                                                              -i- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL. EXTRACELLULAR (POTENTIAL).
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25F68411E3602A12 CRC64;
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                                                                 18.7%; Score 239.5; DB 1
29.5%; Pred. No. 2.8e-13;
tive 32; Mismatches 89
                                                                                                                                                       245 AA
                                                                                                                                                                                                                                                                                                                                                                                                                   Biochim. Biophys. Acta 1399:101-104(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00421; TM4_1; FALSE_NEG.
Transmembrane; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000301; Transmem 4. Pfam; PF00335; transmembrane4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF053454; AAC69711.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27333 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A59260; A59260.
MGD; MGI:1926264; Tm4sf6.
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                                                                                                                                                     STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00259; TMFOUR.
PROSITE; PS00421; TM4 1;
                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               134 ]
245 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                             TM4SF6 OR TSPAN6.
                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                     MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26;
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SEQUENCE
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STRAIN=129/Sv;
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               135 AYRDDIDLQNLIDFAQEYWSCCGARGPNDWNLNIYFNCTDLNPSRERCGVPFSCCVRDPA 194
75 SVLGFAGCIGALRENTFLLKFFSVFLGLIFFLELATGILAFVFKDWIRDQLNFFINNNVK 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 FOEPEVGC---CGKYFLFGFNIVFWVLGALFLAIGLWAWGEKGVLSNISALTDLGGLDPV. 64
                                                                                      -----SGPPSSC-----
                                                                                                                                                                                                                                               16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Platelet-endothelial tetraspan antigen 3 (PETA-3) (CD151 antigen)
                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mamalia, Eutheria, Primates, Catarrhini, Cercopithecidae, Cercopithecinae, Cercopithecinae, Cercopithecinae, Coropithecus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                           Shanmukhappa K., Kapil S.;
"CD151/PETA-3, a tetraspanin molecule, interacts with the 3'
untranslated region and partial nucleoprotein gene of porcine
reproductive and respiratory syndrome virus RNA.";
Submitted (JUN 2000) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18.6%; Score 239; DB 1; Length 25 31.3%; Pred. No. 3.2e-13; ive 30; Mismatches 78; Indels
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EXTRACELLULAR (POTENTIAL).
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CAD2780B63F644A4 CRC64;
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                                                                                                                                                                                                                                                                                                                         Cercopithecus aethiops (Green monkey) (Grivet), and
                                                                                                                                                                                                                      253 AA.
                                                                                     123 HYHSDNSTMKAWDFIQTQLQCCGVNGSSDWT-
                                                                                                                                    161 ----PSGADVQGCYNKAKSWFHSN 180
                                                                                                                  195 MSSTPSVAMMSG----SNWSWSS 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000301; Transmem 4. Pfam; PF00335; transmembrane4; 1 PRINTS; PR00259; TMFOUR.
                                                                                                                                                                                                                                                                                                                                          Macaca mulatta (Rhesus macaque)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF275665; AAF90151.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            242 PC
253 CN
159 N-
28438 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF275666; AAF90152.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PS00421; TM4_1, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                    STANDARD;
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78
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159
153 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                      CERAE
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TRANSMEM
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CARBOHYD
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Blochim. Blophys. Acta 1398:75-85(1998).

-1- SUBCELLUIAR LOCATION: Integral membrane protein.

-1- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.

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                                         62 YILVVAGAVVMYTGVLGCCATFKERRNILRLYFILLLIIFLLEIIAGVLAYVY----YQQ 117
                                                                                                                                                                                         WLFVVVGGVMSVLGFAGCIGALRENTFLLKFFSVFLGLIFFLELATGILAFVFKDWIRDQ 124
                                                                                                                                               LNFFINNNVKAYRDDI------DLQNLIDFAQEYWSCCGARGPNDWNLNIYFNCTD 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fujita S.;
"Molecular cloning and expression of mouse homologue of SFA-1/PETA-3 (CD151), a member of the transmembrane 4 superfamily.";
Biochim. Biophys. Acta 1353:125-130(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C151_MOUSE STANDARD; PRT; 253 AA.
15-50566; 089118;
15-500-1998 (Rel. 36, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
14-0CT-2001 (Rel. 40, Last annotation update)
18-0CT-2001 (Rel. 40, Last annotation update)
19-0CT-2001 (Rel. 40, Last annotation update)
C0T-2001 (Rel. 40, Last annotation update)
C0T-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=97438231; PubMed=9294006;
Hasegawa H., Watanabe H., Nomura T., Utsunomiya Y., Yanagisawa K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fitter S., Seldin M.F., Ashman L.K.; "Characterisation of the mouse homologue of CD151 (PETA-1/SFA-1); genomic structure, chromosomal localisation and identification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleogromi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
POTENTIAL.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98267146; PubMed=9602068;
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EMBL, U89772; AAC25976.1; --
MGD, MGI:1095360; CG151.
InterPro; IPR000301; Transmem_
                                                                                                                                                                                                                                                                                        LNPSRERCGVPFSCC 189
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                                                                                                                                                                                                                                                                                                                                                        LREARGRY-VPDSCC 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         novel splice forms.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
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                                                                                                                                                                                                                             WLPVVVGGVMSVLGFAGCIGALRENTFLLKFFSVFLGLIFFLELATGILAFVFKDWIRDQ 124
                                                                                                                                                                                                                                                                                                 LNFFINNN-----VKAYRDD--IDLQNLIDFAQEYWSCCGARGPNDWNLNIYFNCTDLNP 177
                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                          8 FQEPEVGC---CGKYFLFGFNIVFWVLGALFLAIGLWAWGEKGVLSNISALTDLGGLDPV 64
                                                                                                                                                                                Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL)
G -> S (IN REF. 1).
                                                                                                                            20;
                                                                                      18.6%; Score 239; DB 1; Length 253; 32.3%; Pred, No. 3.2e-13;
                                                                                                      32.3%; Pred. No. 3.ze-zz,
tive 28; Mismatches 82; Indels
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                                                     AEBEEBCE2D765F1B CRC64;
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CYTOPLASMIC (POTENTIAL).
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GO; GO:0005867; C:integral to plasma membrane; TAS.
InterPro; IPR000301; Transmem_4.
Pfam; PF00335; transmembrane4; 1.
PRNUTS; PR00259; TWPCOTR.
PROSITE; PS00421; TM4 1; 1.
Glycoprotein; Transmembrane.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last seq
15-SEP-2003 (Rel. 42, Last anno
                                                     28246 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF089749; AAC35859.1;
                                                                                                                                                                                                                                                                                                                                                                         SRERCGVPFSCC 189
                                                                                                                                                                                                                                                                                                                                                                                                        177 SRV---VPDSCC 185
                                                                                                                          62; Conservative
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253
159
237
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106
224
239
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 243 2
159 1
237 2
253 AA;
                                                                                                        Similarity
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                CARBOHYD
CONFLICT
SEQUENCE
                                                                                      Query Match
Best Local S:
Matches 62
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WEDLINE-21085660; PubMed-11217851;

WEDLINE-21085660; PubMed-11217851;

A MAZAWA T., Shinata A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A MAZAWA T., Hara A., Shibata K., Yoono H., Adachi J., Fukuda S.,

A Azawa R., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Azawa R., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Alzawa R., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Salto T., Okazaki Y., Golobori T., Bono H., Kasukawa T., Saito R.,

A Kuehl P., Lewis S., Matauo T., Nikaido I., Resole G., Quackenbush J.,

A Schriml L.M., Staubli F., Suruki R., Tomita M., Wagner L., Washio T.,

A Schriml L.M., Staubli F., Suruki R., Tomita M., Wagner L., Washio T.,

A Schriml L.M., Staubli F., Suruki R., Tomita M., Gariboldi M.F.,

B Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.F.,

A Uyons P., Marchioni L., Mashima J., Machaserts P.,

Lyons P., Marchioni L., Mashima J., Machaserts P.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
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                                                                                                                                                                                                                                                                                                                                                                                                    15 CCGKYFLFGFNIVFWVLGALFLAIGLWAMGEKGVLSNISALTDLGGLDPVWLFVVVGGVM 74
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                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
4-LINKED (GLCNAC. . .) (POTENTIAL)
DD7BA332BF6584EB CRC64;
                                                                                                                                                                                                                                                                                                    36;
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                                                                                                                                                                       18.4%; Score 236; DB 1; Length 239; 28.0%; Pred. No. 5.4e-13;
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STRAIN-BALB/C; TISSUE-Brain;
Nagira M., Ishikawa K.-I., Fujikawa K., Takagi S., Yoshie O
"Molecular cloning and expression of mouse PE31 (TALLA).";
Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                              91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       193 PAMSSTPSVAMMSGSNWSWSSRAPYTPKAVWASLRSGC 230
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           N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                        30; Mismatches
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                                                     26779 MW;
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                                                                                                                                                                                                                                                                                              61; Conservative
180 1
239 AA;
                                                                                                                                                                                                                                  Local Similarity
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CARBOHYD
SEQUENCE
                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- TISSUE SPECIFICITY: B CELLS, MONOCYTES, MACROPHAGES, NEUTROPHILS,
-1- TISSUE (CD4 OR CD8) POSITIVE THWOCYTES, PERIPHERAL T CELLS.
-1- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
-1- DATABASE: NAME=PROW; NOTE=CD guide CD53 entry;
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd53.htm".
                                                 MEDLINE=91055810; PubMed=1700763; Angelisova M., Horejsi V.; Angelisova P., Vlcek C., Stefanova I., Lipoldova M., Horejsi V.; "The human leucocyte surface antigen CD53 is a protein structurally similar to the CD57 and MRC Ox 44 antigens."; Immunogenetics 32:281-285(1990).
                                                                                                                                                                                                                                                                                                                                                         "Identification and analysis of cDNA clones encoding CD53. A pan-leukocyte antigen related to membrane transport proteins."; J. Immunol. 145:4322-4325(1990).
-:- FUNCTION: MAY BE INVOLVED IN GROWTH REGULATION IN HEMATOPOIETIC
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POTENTIAL.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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31.0%; Pred. No. 5.5e-13;
iive 31; Mismatches 64
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                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=91079522; PubMed=2258620;
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hes 54; Conservative
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Glycoprotein; Antigen; Ti
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PROSITE; PS00421; TM4 1
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Genew; HGNC:1686; CD53.
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148
219 AA;
                 FROM N.A.
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ID _C151_HUMAN
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                     RRARRER RRARRE
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Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtвuki S.,
Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                              "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
R-LINKED (GLCNAC. .) (POTENTIAL).
R-P [IN REP. .)
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01-NOV-1990 (Rel. 16, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Leukocyte surface antigen CD53 (Cell surface glycoprotein CD53)
CD53 OR MOX44.
Homo sapiens (Human)
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . . ) (FN-LINKED (GLCNAC. . 
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EMBL; AF052492; AAC34579.1; ALT INIT.
EMBL; AK004776; BAB23554.1; -.
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InterPro; IPR000301; Transmem 4.
Pfam; PF00335; transmembrane4; 1.
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PROSITE; PS00421; TM4 1; 1.
Glycoprotein; Transmembrane.
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les 51; Conservative
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P19397;
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TRANSMEM
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CONFLICT
SEQUENCE
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CD53_HUMAN
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25; Gaps

DB 1; Length 219; 64; Indels

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or send an email to license@isb-sib.ch)

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TISSUE-COLON, and Kidney;

TYSUE-COLON, and Kidney;

RA STRAUBBERT R.D., Colling F.S., Wagner L.H., Derge J.G.,

RA Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Bobleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,

Rableton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,

Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rabas S.A., McKwann P.J., McKernan K.J., Malek J.A., Gunzarane P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gaby L.J., Hulyk S.W.,

Rachards S., Worley K.C., Hale S., Garcia A.M., Gaby L.J., Hulyk S.W.,

Rachards S., Worley K.C., Hale S., Garcia A.M., Gaby L.J., Hulyk S.W.,

Rachards S., Worley W., Sodergren E.J., Lu X., Gibbs R.A.,

Rachards S.A., McKetteman M., Madan A., Rodrigues S., Sanchez A.,

Rachards A.C., Grimwood J., Schmutz J., Myers R.M.,

Rachiguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rachards A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S. N. Krzywinski M.I., Skalska U., Smailus D.E.,

Racheration and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                         TISSUE=Placelet;
MEDLINE=95359431; PubMed=7632941;
Ritter S., Tetaz T.J., Berndt M.C., Ashman L.K.;
"Molecular cloning of cDNA encoding a novel platelet-endothelial cell
tetra-span antigen, PETA-3.";
Blood 86:1348-1355(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hasegawa H., Utsunomiya Y., Kishimoto K., Yanaqisawa K., Fujita S.; "SPA-1, a novel cellular gene induced by human T-cell leukemia virus type 1, is a member of the transmembrane 4 superfamily.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-!- SUBUNIT: Interacts with integrins alpha3betal, alpha5betal,
alpha3betal and alpha6beta4, with CD9 and CD181.

-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- TISSUE SPECIFICITY: Expressed in a variety of tissues including vascular.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Whittock N.V., McLean W.H.I.; defined mapping, and intragenic corganization, amplification, fine mapping, and intragenic polymorphisms of the human hemidesmosomal tetraspanin CD151 gene."; Biochem. Biophys. Res. Commun. 281.425-430(2001).
                 01-FEB-1996 (Rel. 33, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-Batelet-endothelial tetraspan antigen 3 (PETA-3) (GP27) (Membrane glycoprotein SFA-1) (CD151 antigen)
                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-96186759; PubMed=8627808;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    type 1, is a member of the tree.
J. Virol. 70:3258-3263(1996).
  P48509; Q14826; Q96TE3;
                                                                                                                                                   Homo sapiens (Human).
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=11181065;
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65 WLFVVVGGVMSVLGFAGCIGALRENTFLLKFPSVFLGLIFFLELATGILAFVFKDWIRDQ 124
                      62 YILVVAGTVVMVTGVLGCCATFKERRNLERLYFILLLIFLLEIIAGILAYAY----YQQ 117
                                                                        125 LNFFINNNVKAYRDDID------LQNLIDFAQEYWSCCGARGPNDWNLNIYFNCTD 174
                                                                                                Search completed: November 21, 2003, 13:44:05
                                                                                                                                                175 LNPSRERCG--VPFSCC 189
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INDUCTION: BY HTLV-1.
SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
DATABASE: NAME=PROW; NOTE=CD guide CD151 entry;
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd151.htm".

30;

77; Indels

29; Mismatches

61; Conservative

Local Similarity

Best Loca Matches

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Query Match

18.2%; Score 234; DB 1; Length 253; 31.0%; Pred. No. 8.5e-13;

SC81D7D62D750EAF CRC64;

253 AA; 28313 MW;

SEQUENCE

137

CARBOHYD

DOMAIN

VARIANT VARIANT

CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL)
R -> K.

/FTId=VAR_012490. S -> P. /FTId=VAR_012491

EXTRACELLULAR (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL). POTENTIAL.

18 39 57 78 1112 221 242 253 1159

19 11 11 11 13 13 13 13

TRANSMEM DOMAIN TRANSMEM DOMAIN TRANSMEM

DOMAIN

EXTRACELLULAR (POTENTIAL) Polymorphism. CYTOPLASMIC (POTENTIAL).

POTENTIAL POTENTIAL

; 602243; -. GO:0005887; C:integral to plasma membrane; TAS. GO:0005624; C:membrane fraction; TAS.

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EMBL; AF315942; AAK14179.1; -. EMBL; BC001374; AAK101374.1; -. EMBL; BC013302; AAK13302.1; -. Genew; HGNC:1630; CD151.

EMBL; U14650; AAA87064.1; -. EMBL; D29963; BAA06229.1; -.

InterPro; IPR000301; Transmem 4.
Pfam; PR00335; transmembrane4; 1.
PRNTS; PR00259; TMFOUR.
PROSITE; PS00421; TM4_1; 1.
Glycoprotein; Transmembrane; Polymc DOMAIN

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146 CCTTCGTCAGCCCGCTGGTGAATACCTGCTCTTCTTCTTCAACATGCTCTTCTGGGTGA
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9.2%; Score 234; DB 4; Length 1932;
Best Local Similarity 58.8%; Pred. No. 1.4e-51;
Matches 448; Conservative 0; Mismatches 298; Indels 16;
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LOCATION: (1022)
OTHER INFORMATION: n equals a,t,g, or US-09-482-273-41
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OTHER INFORMATION:
FEATURE:
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Sequence 243, App
Sequence 62, Appl
Sequence 243, Appl
Sequence 19, Appl
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1565, Ap
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                                                              November 21, 2003, 17:14:19; Search time 148 Seconds (without alignments) 7569.124 Million cell updates/sec
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Sequence 4
Sequence 1
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(cgn2_6/ptodata/1/ina/5B_COMB.seq:*
(cgn2_6/ptodata/1/ina/6A_COMB.seq:*
(cgn2_6/ptodata/1/ina/6B_COMB.seq:*
(cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
(cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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US-09-188-930-62
US-09-312-283C-62
US-09-312-283C-62
US-09-312-283C-62
US-09-312-283C-62
US-09-312-283C-62
US-09-313-599-1
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US-08-648-12
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US-08-221-298-12
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Maximum Match 100%
Listing first 45 summaries
                                          - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Gaps

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Sequence 3, Appli
Sequence 7, Appli
Sequence 10430, A
Sequence 10138, A
Sequence 10523, A
Sequence 10523, A
Sequence 2, Appli
Sequence 1, Appli
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Sequence 16, Appl
Sequence 14, Appl
Sequence 5727, Ap
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3 US-08-852-824-3

3 US-09-197-649-7

4 US-09-252-991A-10430

4 US-09-252-991A-10645

4 US-09-252-991A-10645

3 US-09-103-846A-2

9 3 US-09-103-846A-1

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1 US-09-232-149A-1

1 US-09-232-149A-1

1 US-09-232-91A-5713
                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: 71 Human Secreted Proteins
TITLE OF INVENTION: 71 Human Secreted Proteins
FILE REFERENCE: PO130P1
CURRENT APPLICATION NUMBER: US/09/482,273
CURRENT FILING DATE: 2000-01-13
EARLIER APPLICATION NUMBER: PCT/US99/15849
EARLIER FILING DATE: 1999-07-14
EARLIER FILING DATE: 1999-07-15
EARLIER FILING DATE: 1998-07-15
SOPTWARE: Patentin Ver. 2.0
SOPTWARE: Patentin Ver. 2.0
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; Sequence 41, Application US/09482273
; Patent No. 6534631
; GENERAL INFORMATION:
                           ORGANISM: Homo sapiens
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, Sequence 243, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
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US-09-188-930-243
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GAGGCGTCATGTCCGTGCCTGGCTTTGCCGGCTGCATCGGGGCTCTCCGGGAGAACACTT
                                                                                                                      390 TCCTGCTCAAGTTTTTCTCAGTGTTCCTTGGCCTCATCTTCTTCCTGGAGGTGGCAACAG
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Sequence 62, Application US/09188930A

Patent No. 6150502

GENERAL INFORMATION:

APPLICANT: Watson, James D.

APPLICANT: Strachan, Lorna

APPLICANT: Strachan, Matthew

APPLICANT: Ornust, Rene

APPLICANT: Onrust, Rene

TITLE OF INVENTION: Compositions Isolated From Skin Cells

TITLE OF INVENTION: and Methods For Their Use

TITLE OF INVENTION: Compositions 1001c1

CURRENT APPLICATION NUMBER: US/09/188,930A

CURRENT PILING DATE: 1998-11-09

NUMBER OF SEQ ID NOS: 348

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 62

LENGTH: 339
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Pred. No. 2.1e-15;
0; Mismatches 60; Indels
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Best Local Similarity 68.6
Matches 131, Conservative
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US-09-188-930-62
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ORGANISM: 1
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APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Lorna
APPLICANT: Steeman, Matthew
APPLICANT: Orrust, Rene
APPLICANT: Onrust, Rene
APPLICANT: Orrust, Rene
APPLICANT: Orrust, Compositions Isolated From Skin Cells
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: L1000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 243
LENGTH:: 399
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Fatent No. 6573095
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Steeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James G.
APPLICANT: Murison, James G.
TITLE OF INVENTION: Compositions Isolated from Skin Cells
TITLE OF INVENTION: and Methods for Their Use
FILE REFERENCE: 11000.1011c2
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 425
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APPLICANT: Wateon, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Matthew
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Onrust, Rene
TITLE OF INVENTION: Compositions Isolated from Skin Cells
TITLE OF INVENTION: Compositions Isolated from Skin Cells
TITLE OF INVENTION: and Methods for Their Use
FILE REFERENCE: 11000.1011c2
CURRENT APPLICATION NUMBER: US/09/312,283C
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 425
SOFTWARE: FRALSEQ for Windows Version 4.0
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                                                                                                                                Length 399
                                                                                                                              Score 95; DB 4; Length 399
Pred. No. 2.1e-15;
0; Mismatches 60; Indels
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 62 LENGTH: 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-312-283C-243
; Sequence 243, Application US/09312283C
; Patent No. 6573095
                                                                                                                            Query Match 3.7%;
Best Local Similarity 68.6%;
Matches 131; Conservative
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                                                   ; TYPE: DNA
; ORGANISM: Mouse
US-09-312-283C-62

// TYPE: DNA
// ORGANISM: Mouse
US-09-312-283C-243
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Best Local Simi
Matches 131;
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                                                                                                                                                                                 APPLICANT: Dong, Jin-Tang; Barrett,

APPLICANT: Dong, Jin-Tang; Barrett,

TITLE OF INVENTION: DIAGNOSTIC METHODS AND

TITLE OF INVENTION: DIAGNOSTIC METHODS AND

TITLE OF INVENTION: HUMAN METASTASIS SUPPRESSOR GENE KAII

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: ANDRESS:

ADDRESSEE: ANDRESS FINNEGAN, L.L.P.
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Pred. No. 5.8e-08;
0; Mismatches 152; Indels
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/430,225A
FILLING DATE: 28-APR-1995
CLASSIFICATION: 514
ATTORNEY, AGBNT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4172
TELECOMMUNICATION INFORMATION:
TELECHONE: (212) 758-480
TELECAL 421792
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                        Sequence 19, Application US/08430225A
Patent No. 6204000
GENERAL INFORMATION:
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51.1%;
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CITY: NEW YORK
STATE: NEW YORK
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Best Local Similarity 51.1<sup>3</sup>
Matches 159, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY 1
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STRANDEDNESS: single
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US-08-430-225A-19
US-08-430-225A-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               350
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RESULT

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ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto
  CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
SSOTWARE: FastSEQ for Windows Version 3:0
LENGTH: 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: PF-0224 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                          ; LOCATION: (1)....(473)
; OTHER INFORMATION: n = A,T,C or G
US-09-736-457-1565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: (1)...(473)
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                                                                                                                                                                     FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  246 ACTICCGGCAGCAGAIGGAGAATIACCCGAAAAACAACCACACTGNTTCNAICCIGGACA 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                              APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C14
FILE REFERENCE: 20121.478C14
CURRENT APPLICATION NUMBER: US/09/702,705
CURRENT FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 1833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Fan, Liqun
APPLICANT: Wang, Aijun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
2.3%; Score 58.4; DB 4; Length 473;
Best Local Similarity 50.6%; Pred. No. 9.3e-06;
Matches 137; Conservative 0; Mismatches 134; Indels
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                                                                                                                                                                                                                                                                                                                                                                                        FastSEQ for Windows Version 3.0
                   Sequence 1565, Application US/09702705
Patent No. 6504010
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1565, Application US/09736457
Patent No. 6509448
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: misc_feature
; LCCATION: (1)...(473)
; OTHER INFORMATION: n = A,T,C or G
US-09-702-705-1565
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Bangur, Chaitanya S.
Lodes, Michael A.
Fanger, Gary
Vedvick, Tom
Carter, Darrick
Retter, Marc
                                                                            Wang, Tongtong
Bangur, Chaitanya S.
Lodes, Michael A.
                                                                                                                         APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
APPLICANT: Fan. Limm
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Fan, Liqun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
US-09-702-705-1565
                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Fast
SEQ ID NO 1565
LENGTH: 473
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                                                                                                                                     321 TAGTGGTTGGAGGCGTCATGTCCGTGCTGGGCTTTTGCCGGCTGCATCGGGGCTCTCCGGG
                                                                                                                                                                                                                                                                              381 AGAACACTITCCIGCTCAAGITITICICAGIGITCCTIGGCCTCAICTICTTCCTGGAGC
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Patent No. 5863735
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN TRANSMEMBRANE 4 SUPERFAMILY
NUMBER OF SEQUENCES:
ADDRESSEE Incyte Pharmaceuticals, Inc.
       Length 473;
Query Match
2.3%; Score 58.4; DB 4; Length 4
Best Local Similarity 50.6%; Pred. No. 9.3e-06;
Matches 137; Conservative 0; Mismatches 134; Indels
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SOFTWARE: Fasteso for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/807,044
FILING DATE: Herewith
CLASSIFICATION: 530
PRIOR PAPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
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                                            CTTCCTGTTTGGCTTCAACATGTTTTCTGGGTGCTGGGAGCCCTGTTCCTGGCCATCGG
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APPLICANT: Testa, Jacqueline E.
APPLICANT: Quigley, James P.
APPLICANT: Quigley, James P.
APPLICANT: Quigley, James P.
APPLICANT: Quigley, James P.
APPLICANT: Seandel, Marco
TITLE OF INVENTION: MONOCLONAL ANTIBOIDES THAT RECOGNIZE ANTIGENS
TITLE OF INVENTION: ASSOCIATED WITH TUMOR METASTASIS
FILE REFERENCE: SUNY
CURRENT APPLICATION NUMBER: US/09/499,781
CURRENT APPLICATION NUMBER: 09/333,599
PRIOR FILING DATE: 1999-06-15
PRIOR FILING DATE: 1999-06-15
SOFTWARE: PATENTING OF SEQ. 10 NOS: 5
SOFTWARE: PATENTING OF SEQ. 10 NOS: 5
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ORGANISM: Homo sapiens
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; LOCATION: (57)..(815)
US-09-499-781-5
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APPLICANT: Quigley, James P.
APPLICANT: Quigley, James P.
APPLICANT: Seandal, Marco
TITLE OF INVENTION: MONOCLOUAL ANTIBOIDES THAT RECOGNIZE ANTIGENS
TITLE OF INVENTION: ASSOCIATED WITH TUMOR METASTASIS
FILE REPERBUCE: SUNY
CURRENT APPLICATION NUMBER: US/09/313,599
CURRENT PILING DATE: 1999-06-15
SOFTWARE: Patentin Ver. 2.0
SSOFTWARE: Patentin Ver. 2.0
LENGTH: 827
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Patent No. 6245898
GENERAL INFORMATION:
          INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: ILENGTH: 1151 base pairs TYPE: nucleic acid STRANDEDMESS: single TYPE: NCPOLOGY: linear IMMEDIATE SOURCE: LIBRARY: SCORNOTO1 CLONE: 663655
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ORGANISM: Homo sapiens
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; LOCATION: (57)..(815)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    235 CCTCTGGGCCTGGGGTGAGAGGGTGTTCTCTCCAACATCTCTGCGCTGACCGATCTGGG 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               214 carcrigacionacione de actividade 214 carcrigados de 267 carcrigados 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 268 craccioscocacacorracarcorregios de concorrer de conco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         474
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                                                                                                              415 CCTTGGCCTCATCTTCTTCCTGGAGCTGGCAACAGGGATCTTGGCCTTCGTATTCAAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09333599
Patent No. 6245898
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: General James P.
APPLICANT: General Marco
APPLICANT: General Marco
APPLICANT: Seandel, Marco
APPLICANTION: MONOCLONAL ANTIBOIDES THAT RECOGNIZE ANTIGENS
TITLE OF INVENTION: ASSOCIATED WITH TUMOR METASTASIS
FILE REFERENCE: SUNY
CURRENT PILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 5
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                                                                                                                                                                                                                                                               475 CTGGATTCGAGACCAGCTCAATTTCTTCATTAACAACAACGTCA 518
                                                                                                                                                                                                                                                                                                               475 CTGGATTCGAGACCAGCTCAATTTCTTCATTAACAACAACGTCA 518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.3%; Score 57.2; DB 3; 1
Best Local Similarity 48.3%; Pred. No. 2.6e-05;
Matches 195; Conservative 0; Mismatches 203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09499781
Patent No. 6498014
GENERAL INFORMATION:
APPLICANT: Testa, Jacqueline E.
APPLICANT: Quigley, James P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 870
                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
US-09-333-599-1
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US-09-499-781-1
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115 CACCATGCCGGGCAAGCACCACCACTTCCAGGAACCCGAGGTCGGCTGCTGCTGCGGAAATA 174
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APPLICANT: Seandel, Marco
TITLE OF INVENTION: MONOCLONAL ANTIBOIDES THAT RECOGNIZE ANTIGENS
TITLE OF INVENTION: ASSOCIATED WITH TUMOR METASTASIS
FILE REPERENCE: SUNY
CURRENT APPLICATION NUMBER: US/09/499,781
CURRENT FILING DATE: 2000-02-08
PRIOR APPLICATION NUMBER: 09/333,599
PRIOR PILING DATE: 1999-06-15
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2.3%; Score 57.2; DB 4; Length 87
Best Local Similarity 48.3%; Pred. No. 2.6e-05;
Matches 195; Conservative 0; Mismatches 203; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  475 CTGGATTCGAGACCAGCTCAATTTCTTCATTAACAACAACGTCA 518
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Sequence 8, Application US/08705771

GENERAL INFORMATION:

APPLICANT: Paul Moore, Reiner Gentz, Hongjin Ji,

APPLICANT: Jian Ni and Jing-Shan Hu

TITLE OF INVENTION: Human Genes, Sequences and

TITLE OF INVENTION: Expression Products

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

ADDRESSEE: CARCHI, STEMART & OLSTEIN

STREET: 6 BECKER FARM ROAD

STATE: NEW JERSEY

COUNTRY: USA
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MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
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OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO
LENGTH: 870
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; ORGANISM: Homo sapiens
US-09-499-781-1
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TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                   Query Match 2.3%; Score 57.2; DB 3; Length 1 Best Local Similarity 51.3%; Pred. No. 3.2e-05; Matches 162; Conservative 0; Mismatches 148; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-855-140-2

Sequence 2, Application US/08855140

Sequence 2, Application US/08855140

PARENTA INFORMATION:

APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.

TITLE OF INVENTION: NEW TRANSMEMBRANE PROTEIN

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYLE Pharmaceuticals, Inc.
                                                                                                            325800-346 (PF196)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM:
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/855,140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto COUNTRY: USA
NUMBER: US/08/705,771
August 30, 1996
                                                 ATTONNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 3258
TELECOMMUNICATION INFORMATION:
TELEPHONE: 973-994-1744
                                                                                                                                                        INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS: LENGTH: 1344 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    461 CTACACGGACAAGATT 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   466 ATTCAAGGACTGGATT 481
   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear; MOLECULE TYPE: DNA US-08-705-771-8
                  FILING DATE: AUCLASSIFICATION:
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160 CTGCTGCGGGAAATACTTCCTGTTTGGCTTCAACATTGTTTTCTGGGTGCTGGGAGCCCT 219
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Job time : 152 secs
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                                                                                                                                                                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-85-0555
TELEPHONE: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 977 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE:
LIBRARY: MYOMNOT01
CLONE: 779308
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November 21, 2003, 13:43:38; Search time 30 Seconds (without alignments) 1417.879 Million cell updates/sec
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1 MPGKHQHFQEPEVGCCGKYF.....RAPYTPKAVWASLRSGCRTT 233
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              666188 seqs, 182559486 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                              - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Result	¢	Query	•	;	SUMMARIES	
0	Score	Match	Match Length DB ID	8	QI	Description
rd	1283	100.0	233	10	US-09-972-970-4	Segmence 4. Appli
7	1066	83.1	270	10	US-09-934-268-2	Segmence 2. Appli
m	1066	83.1	270	15	US-10-103-196-16	Sequence 16. Appl
4	1066	83.1	270	15	US-10-162-435-36	Semience 36 Appl
S.	885	69.0	271		US-09-925-299-978	Segmence 978
φ	882	69.0	271	11	US-09-925-299-978	Semience 978 Ann
7	791	61.7	268		US-10-103-196-17	Semience 17 April
80	669	54.5			US-09-729-674-170	Segmence 170 ann
o,	638.5	49.8			US-09-796-753-126	Semience 126 Ann
10	638.5	49.8			US-09-905-674-2	Segmence 2 Appli
11	638.5	49.8		11	US-09-892-877-267	Semience 267 App
12	638.5	49.8		11	US-09-948-783-269	Semience 269
13	625.5	48.8		11	US-09-892-877-126	Semience 126 Ann
14	625.5	48.8	270	11	US-09-948-783-127	Segment 127 App
15	619.5	48.3	270	11	US-09-957-187-16	Semience 16 Anni

417-38 Seguence 38,	98-62	71-133 Sequence 13	87-79 Sequence 79,	96-22 Seguence 22,	68-4 Sequence 4,	35-38 Sequence 38,	374-123 Sequence 123	387A-123 Sequence 123	130A-123 Sequence 123	Sequence 276	Sequence 123	49-278 Sequence 278	-278 Sequence 278	278	-278 Sequence 278	92A-123 Sequence 123	53A-123 Sequence 123	89-278 Sequence 278	90-278 Seguence 276	91-278 Seguence 276	92-278	94-278 Sequence 276	98-278 Sequence 278	99-278 Sequence 276	e 278	69-278 Sequence 278	83-278 Sequence 278	87-278 Sequence 278	89-278 Segmence 276
-10-042-	-10-106-	-66	-09-957-	ŗ	-09-934-	-10-	-60	-10-015	-10-006-	-10-199-6	-10-006-1	0-187-7	0-194-	0-184-	10-196-7	US-10-015-3	10-017-2	0-173-6	-10-173-6	0 - 173 -	-10-17	-10-17	-173-	-10-17	US-10-173-7	US-10-174-5	0-174-	US-10-174-5	US-10-174-5
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ALIGNMENTS

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Sequence 4, Application US/09972970

Patent No. US20020164693A1

GENERAL INFORMATION:

APPLICANT: Shi et al.

TITLE OF INVENTION: TM4SF Receptor Polynucleotides, Polypeptides, and Antibodies
FILE REFERENCE: PTOS6P1

CURRENT FILING DATE: 2001-10-10

PRIOR PLIING DATE: 2001-10-10

PRIOR PAPLICATION NUMBER: 06/195,336

PRIOR PELING DATE: 2000-04-10

NUMBER OF SEQ ID NOS: 8

NUMBER OF SEQ ID NOS: 8

SEQ ID NO 4

LENGTH: 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 IRDQLNFFINNNVKAYRDDIDLQNLIDFAQEYWSCCGARGPNDWNLNIYFNCTDLNPSRE 180
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100.0%; Score 1283; DB 10;
Best Local Similarity 100.0%; Pred. No. 9.7e-119;
Matches 233; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
US-09-972-970-4
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FILING DATE: 2002-01-08
APPLICATION NUMBER: US 60/260,286
FILING DATE: 2001-01-08
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Publication No. US20030096305A1
GENERAL INFORMATION:
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                                                    TYPE: PRT; ORGANISM: Homo sapiens
US-10-103-196-16
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  ; SEQ ID NO 16
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TITLE OF INVENTION: TM4SF Polynucleotides, Polypeptides, and Antibodies
FILE REFREENCE: PTOORSP1
CURRENT APPLICATION NUMBER: US/10/103,196
CURRENT FILING DATE: 2002-03-22
PRIOR PILING DATE: 2000-01-09
RRIOR FILING DATE: 2000-01-109
RRIOR FILING DATE: 2000-05-18
RRIOR FILING DATE: 2000-01-28
RRIOR FILING DATE: 2000-01-28
RRIOR FILING DATE: 2000-01-28
RRIOR PILING DATE: 2000-01-28
RRIOR PILING DATE: 1999-06-11
RRIOR PILING DATE: 1999-06-11
RRIOR PILING DATE: 1999-06-03
RRIOR PILING DATE: 1900-06-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 LDPVWLFVVVGGVMSVLGFAGCIGALRENTFLLKFFSVFLGLIFFLELATGILAFVFKDW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 IRDQLNFINNNVKAYRDDIDLQNLIDFAQEYWSCCGARGPNDWNLNIYFNCTDLNPSRE 180
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  RCGVPFSCCVRDPAMSSTPSVAMMSGSNWSWSSRAPYTPKAVWASLRSGCRTT 233
                              181 RCGVPFSCCVRDPAMSSTPSVAMMSGSNWSWSSRAPYTFKAVWASLRSGCRTT 233
                                                                                                                                                              Sequence 2, Application US/09934268

Sequence 2, Application US/09934268

Setenct No. US20020172986A1

GENERAL INFORMATION:
APPLICANT: Leiby, Kevin R.
TITLE OF INVENTION: MEMBER AND USES THEREOF

FILE REFERENCE: 10448-079001

CURRENT APPLICATION NUMBER: US/09/934,268

CURRENT FILING DATE: 2001-08-21

FRIOR APPLICATION NUMBER: 60/226,612

PRIOR APPLICATION NUMBER: 60/226,612

RIOR FILING DATE: 2000-08-21

NUMBER OF SEQ ID NOS: 4

SEQ ID NO 2

LENGTH: 270
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Best Local Similarity
Matches 193; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: HOI
US-09-934-268-2
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61 LDPVWLFVVVGGVMSVLGFAGCIGALRENTFLLKFFSVFLGLIFFLELATGILAFVFKDW 120
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GERMEAL INFORMATION:
GERMEAL INFORMATION:
GULTIS. Rachel
APPLICANT: Glucksmann, Maria Alexandra
APPLICANT: Cutris., Rory A. J.
APPLICANT:
Editor:
APPLICANT: Bandaru, Rajasekhar
APPLICANT:
Bandaru, Rajasekhar
APPLICANT:
Bandaru, Rajasekhar
APPLICANT:
Bandaru, Rajasekhar
APPLICANT:
Bandaru, Rajasekhar
APPLICANT:
BANDRICANT:
ILILB OF INVENTION:
CELL SURRACE PROTEIN FAMILY MEMBERS
FILE REFERENCE:
10448-189001
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/10/162,435
CURRENT APPLICATION NUMBER: US 60/197,507
PRIOR FILING DATE: 2001-04-17
PRIOR PLING DATE: 2001-04-18
PRIOR PLING DATE: 2001-06-25
PRIOR PLING DATE: 2001-06-25
PRIOR PLING DATE: 2001-06-25
PRIOR PLING DATE: 2001-06-25
PRIOR PLING DATE: 2001-06-23
PRIOR PLING DATE: 2001-06-24
PRIOR APPLICATION NUMBER: US 60/205,674
PRIOR PLING DATE: 2001-06-19
PRIOR PLING DATE: 2001-06-19
PRIOR PLING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: US 60/205,674
PRIOR PLING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: US 60/205,674
PRIOR PLING DATE: 2001-06-21
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        Length 270;
                                                                                Indels
Query Match 83.1%; Score 1066; DB 15; Best Local Similarity 99.5%; Pred. No. 3.2e-97; Matches 193; Conservative 0; Mismatches 1;
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PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 10/041,406
PRIOR FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: PCT/US02/00275
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; Sequence 17, Application US/10103196; Publication No. US20030050466A1; GENERAL INFORMATION:
                         182 RCGVPFSCCTKDPA 195
          181 RCGVPFSCCVRDPA 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 155; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens
US-09-925-299-978
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 978, Application US/09925299; Sequence 978, Application US/09925299; Patent No. US20020055627A1; GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies; FILS REFERENCE: PA102

CURRENT APPLICATION NUMBER: US/09/925,299; CURRENT FILING DATE: 2001-08-10; PRIOR APPLICATION NUMBER: PCT/US00/05883; PRIOR APPLICATION NUMBER: PO1124,270; PRIOR FILING DATE: 1999-03-12; NUMBER OF SEQ ID NOS: 1556; SOFFWARE: Patentin Ver: 2.0; SEQ ID NO 978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69.0%; Score 885; DB 9; Length 271; 79.9%; Pred. No. 2.5e-79; Live 16; Mismatches 21; Indel8
PRIOR APPLICATION NUMBER: US 09/914,268
PRIOR FILING DATE: 2001-08-21
PRIOR FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/USO1/41811
PRIOR PRING DATE: 2000-08-21
PRIOR PRING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: PRICE TO NOS: 38
LENGTH: 270
TYPE: PRT
VORGANISM: Homo sapiens
US-10-162-435-36
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ORGANISM: Homo sapiens
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US-09-925-299-978
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APPLICANT: NI et al.

TITLE OF INVENTION: TM4SF Polynucleotides, Polypeptides, and Antibodies
TITLE OF INVENTION NUMBER: US/10/103,196
CURRENT APPLICATION NUMBER: US/10/103,196
CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: POJ/707,936
PRIOR PILING DATE: 2000-01-08
PRIOR PILING DATE: 2000-01-18
PRIOR PILING DATE: 2000-01-28
PRIOR PILING DATE: 2000-01-28
PRIOR PILING DATE: 1999-06-18
PRIOR PILING DATE: 1999-06-11
PRIOR PILING DATE: 1999-06-11
PRIOR PILING DATE: 1999-06-01
PRIOR PILING DATE: 1999-06-03
PRIOR PILING DATE: 1999-06-19
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Sequence 978 Application US/09925299; Bublication No. US20030040617A9; GENERAL INFORMATION:
APPLICANT: ROBEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REFERENCE: PAIO2
CURRENT FILING DATE: 2001-08-10; PRIOR APPLICATION NUMBER: US/09/925,299; CURRENT FILING DATE: 2000-03-08; PRIOR FILING DATE: 1999-03-12; NUMBER OF SEQ ID NOS: 1556; NUMBER OF SEQ ID NOS: 1556; SOFTWARE PATENTIN VET. 2.0
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121 IRDOLNFFINNNVKAYRDDIDLONLIDFAQBYWSCCGARGPNDWNLNIYFNCTDLNPSRE 180
                                                                                                                                                           181 RCGVPFSCCVRDPA-----MSSTPSVAMMSGSNWSWSSR
                                                                                                                               Sequence 126, Application US/09796753
Publication No. US20030027998A1
GENERAL INFORMATION:
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US-09-796-753-126
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                                                                                                                              1 MPGKHQHFQEPEVGCCGKYFLFGFNIVFWVLGALFLAIGLWAWGEKGVLSNISALTDLGG 60
                                                                                                                                           1 MSGK--HYKGPEVSCCIKYFIFGFNVIFWFLGITFLGIGLWAWNEKGVLSNISSITDLGG 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Fechtel, Kim
APPLICANT: Fechtel, Kim
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: 6055-647
CURRENT APPLICATION NUMBER: US/09/729,674
CURRENT FILING DATE: 2000-12-04
PRIOR FILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 283
SOFTWARE: Patentin Ver. 2.0
                                                                                                         Gaps
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Best Local Similarity 62.9%; Pred. No. 3.9e-61;
Matches 139; Conservative 16; Mismatches 30; Indels 36;
                                                                              Query Match 61.7%; Score 791; DB 15; Length 268; Best Local Similarity 72.2%; Pred. No. 4.7e-70; Matches 140; Conservative 16; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              Merberg, David
Treacy, Maurice
Agostino, Michael J.
Steininger II, Robert J.
Spanlding, Vikki
Wong, Gordon G.
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                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Jacobs, Kenneth
MCCOV, John M.
APPLICANT: LaVallie, Edward R.
APPLICANT: Collins-Racie, Lisa A.
                                                                                                                                                                                                                                                                       181 RCGVPFSCCVRDPA 194
                                                                                                                                                                                                                                                                                            179 RCGVPFSCCTKDPA 192
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 17
LENGTH: 268
TYPE: PRT
ORGANISM: Homo sapiens
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US-09-729-674-170
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US-09-729-674-170
                                                          US-10-103-196-17
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Sequence 269, Application US/09948783
Publication No. US20030100051A1
GENERAL INFORMATION:
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Matches 119; Conservative
                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                           182
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                                                                                                                                                                                               62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 PREFFESNIKSYRDDIDLQNLIDSLQKANQCCGAYGPEDWDLNVYFNCSGASYSREKCGV 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183 PFSCCVPDPAQKVVNTQCGYDVRIQLKŠKWDESIFTKGCIQALEŠWLPRNIYIVAGVFIA 242
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                                                                                                                                                            5 HOHFQEPEVGCCGKYFLFGFNIVFWVLGALFLAIGLWAWGEKGVLSNISALTDLGGLDPV
                                                                                                                                                                                3 YYRYSNAKVSCWYKYLLFSYNIIFWLAGVVFLGVGLWAWSEKGVLSDLTKVTRMHGIDPV
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                                                                                                                                Gaps
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                                                                                      Query Match

49.8%; Score 638.5; DB 11; Length 270;
Best Local Similarity 49.4%; Pred. No. 5.5e-55;
Matches 119; Conservative 37; Mismatches 66; Indels 19;
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Fublication No. US20030039647A1
GENERAL INFORMATION:
APPLICANT: Reinhard Christoph
APPLICANT: Reinhard, Pablo
TITLE OF INVENTION: TETRASPAN PROTEIN AND USES THEREOF
FILE REFERENCE: PP-01700.002/200130.521
CURRENT APPLICATION NUMBER: US/08/905,674
CURRENT FILING DATE: 2001-07-13
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 2
LENGTH: 270
; LENGTH: 270
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-753-126
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US-09-905-674-2
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Sequence 267, Application US/09892877

Sequence 267, Application US/09892877

Publication No. US20030077809A1

GENERAL INFORMATION:

TAPLICANT: RUDEN et. al.

TITLE OF INVENTION: 97 Human secreted proteins

FILE REPERENCE: PZ028P1

CURRENT FILING DATE: 2001-06-28

PRIOR PILING DATE: EARLIER APPLICATION NUMBER: US/09/437,658

PRIOR FILING DATE: EARLIER FILING DATE: 1999-11-10

NUMBER OF SEQ ID NOS: 461

SOFTWARE: PATENTIN Ver. 2.0

SEQ ID NO 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 HOHFOEPEVGCCGKYFLFGFNIVFWVLGALFLAIGLWAWGEKGVLSNISALTDLGGLDPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 270;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49.8%; Score 638.5; DB 11;
49.4%; Pred. No. 5.5e-55;
ive 37; Mismatches 66;
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TITLE OF INVENTION: 97 Human secreted proteins
FILE REFERENCE: PZ028P2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT PELICATION NUMBER: US/09/948,783
CURRENT PELING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 06/231,846
PRIOR FILING DATE: 2000-09-11
PRIOR FILING DATE: 2000-09-11
PRIOR PELING DATE: 2001-66-28
PRIOR PELING DATE: 1001-66-28
PRIOR PELING DATE: 1999-11-10
PRIOR PELING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: 09/437,658
PRIOR PELING DATE: 1999-06-06
PRIOR PELING DATE: 1999-05-12
PRIOR PELING DATE: 1998-05-12
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Gaps

19;

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123 FREFFESNIKSYRDDIDLQNLIDSLQKANQCCGAYGPEDWDLNVYFNCSGASYSREKCGV 182
                                                                                                                                                                                                                                                                                                        125 LNFFINNNVKAYRDDIDLQNLIDFAQEYWSCCGARGPNDWNLNIYFNCTDLNPSRERCGV 184
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                                                                                                                                                                                           3 YYRYSNAKVSCWYKYLLFSYNIIFXLAGVVFLGVGLWAWSEKGVLSDLTKVTRMGIDPV 62
                                                                                                                                                       5 HQHFQEPEVGCCGKYFLFGFNIVFWVLGALFLAIGLWAWGEKGVLSNISALTDLGGLDPV
                                    Length 270;
                                                                                                67; Indels
                                    DB 11;
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CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 05/892,877
PRIOR APPLICATION NUMBER: 09/892,877
PRIOR PLING DATE: 2000-09-11
PRIOR PLING DATE: 2000-09-13
PRIOR PLING DATE: 1999-11-10
PRIOR PLING DATE: 1999-11-10
PRIOR PLING DATE: 1999-05-06
PRIOR PLING DATE: 1999-05-06
PRIOR PLING DATE: 1999-05-12
PRIOR PLING DATE: 1999-05-13
PRIOR PLING DATE: 1999-05-13
PRIOR PLING DATE: 1999-05-18
                                    Query Match 48.8%; Score 625.5; DB 1 Best Local Similarity 49.0%; Pred. No. 1.1e-53; Matches 118; Conservative 37; Mismatches 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 127, Application US/09948783
Publication No. US20030100051A1
GENERAL INFORMATION:
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. OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-892-877-126
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TITLE OF INVENTION: 97 Human secreted proteins
FILE REFERENCE: P2028P1
CURRENT APPLICATION NUMBER: US/09/892,877
CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/437,658
PRIOR FILING DATE: EARLIER FILING DATE: 1999-11-10
NUMBER OF SEQ ID NOS: 461
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 126
LENGTH: 270
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49.8%; Score 638.5; DB 1
Best Local Similarity 49.4%; Pred. No. 5.5e-55;
Matches 119; Conservative 37; Mismatches 66
                        PRIOR APPLICATION NUMBER: 60/085,906
PRIOR FILING DATE: 1998-05-18
PRIOR FILING DATE: 1998-05-18
PRIOR PELING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: 60/085,922
PRIOR APPLICATION NUMBER: 60/085,921
PRIOR APPLICATION NUMBER: 60/085,921
PRIOR FILING DATE: 1998-05-18
PRIOR FILING DATE: 1998-05-18
PRIOR FILING DATE: 1998-05-18
PRIOR PLING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: 60/085,925
PRIOR PLING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: 60/085,928
PRIOR PLING DATE: 1998-05-18
PRIOR PLING DATE: 1998-05-18
PRIOR FILING DATE: 1998-05-18
PRIOR FILING DATE: 1998-05-18
PRIOR FILING DATE: 1998-05-18
NUMBER OF SEQ ID NOS: 465
NUMBER OF SEQ ID NOS: 465
FILING DATE: 1998-05-18
APPLICATION WINDHER: 60/085,906
FILING DATE: 1998-05-18
APPLICATION NUMBER: 60/085,924
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Publication No. US20030077809A1
GENERAL INFORMATION:
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US-09-948-783-269
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ORGANISM: Homo sapiens
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243 I 243
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NAME/KEY: SITE
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LENGTH: 270
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TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: Xaa equals any of the naturally occurring L-amino acids
US-09-948-783-127
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US-09-97-187-16

Sequence 16, Application US/09957187

Publication No. US20030054514A1

GENERAL INFORMATION:
APPLICANT: Shinkers, Richard A.
APPLICANT: LAROchelle, William
ITILE OF INVENTION: NOVEL POLYNUCLEOTIDES AND PROTEINS ENCODED THEREBY
FILE REFERENCE: 1596-540 CIP
CURRENT FILING DATE: 2006-09-19

PRIOR APPLICATION NUMBER: 60/123,667

PRIOR PELING DATE: 1999-03-09

PRIOR PLING DATE: 2000-03-09

PRIOR PLING DATE: 2000-09-20

PRIOR PLING DATE: 2000-09-19

PRIOR PLING DATE: 2000-01-04

NUMBER OF SEQ ID NOS: 85

SEQ ID NO 16

LENGTH: 270

LENGTH: 270
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                                                                                                                                                                                                                                                                                                                                                           3 YYRYSNAKVSCWYKYLLFSYNIIFXLAGVVFLGVGLWAWSEKGVLSDLTKVTRMHGIDPV 62
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                                                                                                                                                                                                                      Query Match
48.8%; Score 625.5; DB 11; Length 270;
Best Local Similarity 49.0%; Pred. No. 1.1e-53;
Matches 118; Conservative 37; Mismatches 67; Indels 19; Gaps
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48.3%; Score 619.5; DB 11; Length 270;
Best Local Similarity 48.1%; Pred. No. 4.2e-53;
Matches 116; Conservative 37; Mismatches 69; Indels 19; Gaps
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; ORGANISM: Homo sapiens
US-09-957-187-16
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243 I 243
LENGTH: 270
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65 WLFVVVGGVMSVLGFAGCIGALRENTFLLKFFSVFLGLIFFLELATGILAFVFKDWIRDQ 124

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        Qy
        125 INFPINNVKAYRDDIDLONLIDPAQEYWSCCGARGPNDWNLNIYFNCTDLNPSRERCGV 184

        Db
        123 FREFFESNIKSYRDDIDLONLIDSLQKANQCCGAYGPEDWDLNVYFNCSGASYSREKCGV 182

        Qy
        185 PFSCCVRDPAMSSTPS-----VAMMSGSNW-------SWSSBAPYTPKAVWAS 225

        Db
        183 PFSCCVRDPAQKVVNTQCGYDVRIQLKSKWDESIFTKGCIQALESWLPRNIYIVACVFIA 242

        Qy
        226 L 226

        Db
        243 I 243

        Search completed: November 21, 2003, 13:46:43

        Job time: 31 secs
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63 VLVLMVGAVMFTLGFAGRVGARRENICLLNPFCGTIVLIFFLELAVAVLAFLFODWVRDR 122

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Sequence 153, Appli Sequence 1, Appli Sequence 4, Appli Sequence 3, Appli Sequence 3, Appli Sequence 205, Appli Sequence 10, Appli Sequence 10, Appli Sequence 20, Appli Sequence 125, Appli Sequence 1, Appli
                                                                                                                                                                                                            November 21, 2003, 17:20:09; Search time 770 Seconds (without alignments) 10772.341 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
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1: /cgn2_6/ptodata/1/pubpna/US07 PUBCOMB.seq:*
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24 254.4 10.0 816 11 US-09-991-053-78 Sequence 25 554.4 10.0 816 11 US-09-957-188 Sequence 27 234 9.2 1932 11 US-106.698-2019 Sequence 27 234 9.2 1932 11 US-106.698-2019 Sequence 28 231.6 9.1 361 11 US-09-984-271-41 Sequence 30 200.2 7.9 360 11 US-09-918-995-37420 Sequence 31 152.4 6.0 476 11 US-09-918-995-37648 Sequence 31 152.4 6.0 476 11 US-09-918-995-37648 Sequence 31 128 5.0 1772 11 US-09-918-995-37537 Sequence 31 128 5.0 1772 11 US-09-918-995-36537 Sequence 32 126.2 5.0 1778 12 US-10-105-384-122 Sequence 33 126.2 5.0 1778 12 US-10-015-3874-122 Sequence 40 126.2 5.0 1778 12 US-10-194-457-277 Sequence 41 126.2 5.0 1778 12 US-10-194-457-277 Sequence 41 126.2 5.0 1778 12 US-10-194-457-277 Sequence 42 126.2 5.0 1778 12 US-10-194-457-277 Sequence 43 126.2 5.0 1778 12 US-10-194-457-277 Sequence 44 126.2 5.0 1778 12 US-10-184-457-277 Sequence 44 126.2 5.0 1778 12 US-10-194-457-277 Sequence 45 126.2 5.0 1778 12 US-10-194-457-277 Sequence 5.0 1778 12 US-10-194-57-277 Sequence 5.0 1778 12 US-10-194-57-27	24 224.4 10.0 816 11 UG-09-991-053-78 Sequence 78, Appl C 25 254.4 10.0 816 11 UG-09-991-053-78 Sequence 78, Appl C 26 240 9.1 819 11 UG-09-961-2019 Sequence 2019, Appl 27 24 9.2 1932 11 UG-09-918-2019 Sequence 2019, Appl 29 230 9.1 361 11 UG-09-918-995-1742 Sequence 37420, A 30 11 UG-09-918-995-777 Sequence 37420, A 31 12.0 200.2 7.9 360 11 UG-09-918-995-777 Sequence 37648, A 31 12.0 2.0 2.7 476 11 UG-09-918-995-1968 Sequence 37648, A 31 12.0 5.0 1772 14 UG-09-918-995-1968 Sequence 3637, Appl 39 126.2 5.0 1778 12 UG-10-918-995-198 Sequence 122, Appl 39 126.2 5.0 1778 12 UG-10-918-995-198 Sequence 122, Appl 40 126.2 5.0 1778 12 UG-10-914-45-277 Sequence 277, Appl 41 126.2 5.0 1778 12 UG-10-194-45-277 Sequence 277, Appl 44 126.2 5.0 1778 12 UG-10-194-45-277 Sequence 277, Appl 44 126.2 5.0 1778 12 UG-10-194-45-277 Sequence 277, Appl 44 126.2 5.0 1778 12 UG-10-194-45-277 Sequence 277, Appl 44 126.2 5.0 1778 12 UG-10-194-45-277 Sequence 277, Appl 44 126.2 5.0 1778 12 UG-10-194-45-277 Sequence 277, Appl 45 126.2 5.0 1778 12 UG-10-197-777 Sequence 277, Appl 45 126.2 5.0 1778 12 UG-10-197-777 Sequence 277, Appl 45 126.2 5.0 1778 12 UG-10-197-777 Sequence 277, Appl 45 126.2 5.0 1778 12 UG-10-197-777 Sequence 277, Appl 45 126.2 5.0 1778 12 UG-10-197-777 Sequence 277, Appl 45 126.2 5.0 1778 12 UG-10-197-777 Sequence 277, Appl 45 126.2 5.0 1778 12 UG-10-197-777 Sequence 277, Appl 45 126.2 5.0 1778 12 UG-10-197-777 Sequence 277, Appl 45 126.2 5.0 1778 12 UG-10-197-777 Sequence 277, Appl 45 126.2 5.0 1778 12 UG-10-197-777 Sequence 277, Appl 45 126.2 5.0 1778 12 UG-10-197-777 Sequence 277, Appl 45 126.2 5.0 1778 12 UG-10-197-777 Sequence 277, Appl 45 126.2 5.0 1778 12 UG-10-197-777 Sequence 277, Appl 45 126.2 5.0 1778 12 UG-10-197-777 Sequence 277, Appl 45 126.2 5.0 1778 12 UG-10-197-777 Sequence 277, Appl 45 126.2 5.0 1778 12 UG-10-197-777 Sequence 277, Appl 45 126.2 5.0 1778 12 UG-10-197-777 Sequence 277, Appl 47 UG-10-10-10-10-10-10-10-10-10-10-10-10-10-	23	294.2	11.6	368	13	-10-042-417		37, Appl
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234 9.2 1932 11 US-09-984-271-41 Sequence 231.6 9.1 361 11 US-09-918-995-37420 Sequence 230.2 7.9 360 11 US-09-918-995-3731 Sequence 200.2 7.9 360 11 US-09-918-995-3731 Sequence 152.4 6.0 476 11 US-09-918-995-3198 Sequence 130.8 5.0 476 11 US-09-918-995-3198 Sequence 130.8 5.0 1772 14 US-10-103-196-7 Sequence 126.2 5.0 1778 12 US-10-9946-3122 Sequence 126.2 5.0 1778 12 US-10-9946-3122 Sequence 126.2 5.0 1778 12 US-10-196-77 Sequence 126.2 5.0 1778 12 US-10-196-127 Sequence 126.2 5.0 1778 12 US-10-199-672-277 Sequence 126.2 5.0 1778 12 US-10-199-672-277 Sequence 126.2 5.0 1778 12 US-10-199-672-277 Sequence 126.2 5.0 1778 12 US-10-194-45-277 Sequence 126.2 5.0 1778 12 US-10-194-572-7 Sequence 126.2 5.0 1778 12 US-10-194-52-77 Sequence 126.2 5.0 1778 12 US-10-194-53-77 Sequence 126.2 5.0	27 234 9.2 1932 11 US-09-984-271-41 Sequence 41, Appl 29 231.6 9.1 361 11 US-09-918-995-3731 Sequence 374.0, A 29 23 230 9.1 411 IU US-09-918-995-3731 Sequence 374.0, A 30 200.2 7.9 360 11 US-09-918-995-3731 Sequence 374.8, A 31 152.4 6.0 476 11 US-09-918-995-3739 Sequence 37648, A 32 130.8 5.2 476 11 US-09-918-995-36537 Sequence 7, Appl 31 122.4 5.0 1772 11 US-09-918-995-36537 Sequence 7, Appl 35 126.2 5.0 1772 11 US-09-918-996-358 Sequence 122, Appl 36 126.2 5.0 1778 12 US-10-199-672-27 Sequence 122, Appl 37 126.2 5.0 1778 12 US-10-199-672-77 Sequence 122, Appl 40 126.2 5.0 1778 12 US-10-199-672-77 Sequence 277, Appl 41 126.2 5.0 1778 12 US-10-199-672-77 Sequence 277, Appl 44 126.2 5.0 1778 12 US-10-194-642-277 Sequence 277, Appl 44 126.2 5.0 1778 12 US-10-194-642-277 Sequence 277, Appl 44 126.2 5.0 1778 12 US-10-194-642-277 Sequence 277, Appl 44 126.2 5.0 1778 12 US-10-194-642-277 Sequence 277, Appl 44 126.2 5.0 1778 12 US-10-194-642-277 Sequence 277, Appl 44 126.2 5.0 1778 12 US-10-194-642-277 Sequence 122, Appl 44 126.2 5.0 1778 12 US-10-194-642-277 Sequence 277, Appl 45 126.2 5.0 1778 12 US-10-194-642-277 Sequence 277, Appl 47 126.2 5.0 1778 12 US-10-194-642-277 Sequence 277, Appl 47 126.2 5.0 1778 12 US-10-194-642-277 Sequence 277, Appl 47 126.2 5.0 1778 12 US-10-194-642-277 Sequence 277, Appl 47 126.2 5.0 1778 12 US-10-1017-253A-122 Sequence 122, Appl 47 126.2 5.0 1778 12 US-10-114-45-277 Sequence 122, Appl 47 126.2 5.0 1778 12 US-10-114-45-277 Sequence 122, Appl 47 126.2 5.0 1778 12 US-10-114-45-277 Sequence 122, Appl 47 126.2 5.0 1778 12 US-10-114-45-277 Sequence 122, Appl 47 126.2 5.0 1778 12 US-10-114-45-277 Sequence 122, Appl 47 126.2 5.0 1778 12 US-10-114-45-277 Sequence 122, Appl 47 126.2 5.0 1778 12 US-10-114-45-277 Sequence 122, Appl 47 126.2 5.0 1778 12 US-10-114-45-277 Sequence 122, Appl 47 126.2 5.0 1778 12 US-10-114-45-45-277 Sequence 122, Appl 47 126.2 5.0 1778 12 US-10-114-45-45-277 Sequence 122, Appl 47 126.2 5.0 1778 12 US-10-114-45-45-277 Sequence 122, Appl 47 126.2 5.0 1778 12 US-10-1		240	9.5	839	14	~		2019, Ap
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US-05-3/2-3/0-2 ; Sequence . 2 Application US/09972970 ; GENERAL INFORMATION:	; TITLE OF INVENTION: TM4SF Receptor Polynucleotides, Polypeptides, and Antibodies	, APPLI	CANT: Sh	ıi et a					
US-07-576-570-2 ; Sequence 2. Application US/09972970 ; Datent No. US20020164693A1 ; GENERAL INFORMATION: ; APPLICANT: Shi et al.		; TITLE	OF INVE	NTION:	TM4SF	Rece	aptor Polynucleotides,	Polypeptides, a	nd Antibodies

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NAME/KEY: misc_feature

OTHER INFORMATION: Incyte ID No. US20030190640A1 234056.5
US-10-252-157-153
                                                                                                                                                                       Sequence 153, Application US/10252157
Publication No. US20030190640A1
GENERAL INFORMATION:
APPLICANT: Farafion:
APPLICANT: Pearson, Cecelia I.
TITLE OF INVENTION: GENES EXPRESSED IN PROSTATE CANCER:
FILE REFRENCE: PA-0027-1 US
CURRENT APPLICATION NUMBER: US/10/252,157
CURRENT APPLICATION NUMBER: 60/295,048
PRIOR FILING DATE: 2001-05-31
NUMBER OF SEQ ID NOS: 501
SOFTWARE: PERL PROGram
SEQ ID NO 153
LENGTH: 2461
                                                                                         2521 AAAAAAAAAAAAA 2538
                                                                                                        2521 AAAAAAAAAAAAAAA 2538
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 1775; Conserv
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                                                                                                                                            31.1%; Score 790.4; DB 10; 92.3%; Pred. No. 7.2e-220; iive 0; Mismatches 66;
PRIOR FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 1
LENGTH: 3184
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                           Query Match
Best Local Similarity 92.3
Matches 855; Conservative
                                                                               FEATURE:
NAME/KEY: CDS
LOCATION: (168)...(977)
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US-09-934-268-1
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Patent No. US20020172986A1
GENERAL INFORMATION:
TITLE OF INVENTION: 23228, A NOVEL HUMAN TETRASPANIN FAMILY
TITLE OF INVENTION: MEMBER AND USES THEREOF
FILE REFERENCE: 10448-07900.1
CURRENT APPLICATION NUMBER: US/9934,268
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: 60/226,612
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GENERAL INFORMATION: APPLICANT: Ni et al.
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          855; Conservative
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Pred. No. 7.2e-220;
                                                                  ACATCAAGGCAGTGAAGGCCAACTGG 924
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                                                                                            Sequence 35, Application US/10162435 Publication No. US20030096305A1 GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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Fatent No. US20020172986A1
GRERAL INFORMATION:
TITLE OF INVENTION: 23228, A NOVEL HUMAN TETRASPANIN FAMILY
TITLE OF INVENTION: MEMBER AND USES THEREOF
FILE REPERRACE: 10448-0.79001
CURRENT APPLICATION NUMBER: US/09/934,268
CURRENT FILING DATE: 2001-08-21
FRIOR APPLICATION NUMBER: 60/226,612
FRIOR APPLICATION NUMBER: 60/226,612
FRIOR FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 813
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Pred. No. 8.7e-197;
0; Mismatches 51;
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Best Local Similarity 93.2%;
Matches 755; Conservative (
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; ORGANISM: Homo sapiens
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TITLE OF INVENTION: TW4SF Polynucleotides, Polypeptides, and Antibodies FILE REFERENCE: PT008P1
CURRENT APPLICATION NUMBER: US/10/103,196
CURRENT FILING DATE: 2002-03-22
PRIOR PLING DATE: 2000-11-08
PRIOR PLING DATE: 2000-11-08
PRIOR PLING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: PCT/US00/13504
PRIOR PILING DATE: 2000-05-18
PRIOR PLING DATE: 2000-05-18
PRIOR PLING DATE: 1099-08-18
PRIOR PLING DATE: 1099-06-11
PRIOR PLING DATE: 1999-06-11
PRIOR PLING DATE: 1999-06-11
PRIOR PLING DATE: 1999-06-11
PRIOR PLING DATE: 1999-06-11
PRIOR PLING DATE: 1999-06-13
PRIOR PLING DATE: 1999-06-19
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Best Local Similarity 92.6
Matches 850; Conservative
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US-10-103-196-4
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PRIOR APPLICATION NUMBER: PCT/US02/00275
PRIOR FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US 60/260,286
PRIOR FILING DATE: 2001-08-01
PRIOR FILING DATE: 2001-08-21
PRIOR FILING DATE: 2001-08-21
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PRIOR FILING DATE: 2000-08-21
PRIOR PILING DATE: 2000-08-21
PRIOR PILING DATE: 2000-08-21
PRIOR PILING DATE: 2000-08-21
PRIOR PILING DATE: 2000-08-21
SEQ ID NOS: 38
SOFTWARE: FREES ID NOS: 38
                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 755; Conservative
                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                            US-10-162-435-37
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                                                                 721 GICTICATGGGCATCGCCCCCCCCAGAACTTIGGCATCTCGCCTGGCCCAGAACCTCGTG
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APPLICANT: Meyers, Rachel

APPLICANT: Gulvésmann, Maria Alexandra

APPLICANT: Gulvésmann, Maria Alexandra

APPLICANT: Gulvésmann, Rary A. J.

APPLICANT: Bandaru, Rajaekhar

FILE REPERBENCE: 10448-18901

CURRENT FILING DATE: 2001-04-17

PRIOR APPLICATION NUMBER: US 09/891,008

PRIOR FILING DATE: 2001-04-18

PRIOR APPLICATION NUMBER: PCT/US01/19963

PRIOR APPLICATION NUMBER: PCT/US01/19963

PRIOR APPLICATION NUMBER: US 09/860,868

PRIOR APPLICATION NUMBER: US 09/860,868

PRIOR PILING DATE: 2000-06-23

PRIOR APPLICATION NUMBER: US 09/866,429

PRIOR PILING DATE: 2001-06-18

PRIOR PILING DATE: 2001-06-21

PRIOR PILING DATE: 2001-06-21

PRIOR PILING DATE: 2001-06-21

PRIOR PILING DATE: 2001-06-21

PRIOR APPLICATION NUMBER: US 06/205,674

PRIOR PILING DATE: 2001-06-21

PRIOR APPLICATION NUMBER: US 06/213,963

PRIOR PILING DATE: 2001-06-21

PRIOR APPLICATION NUMBER: US 06/213,963

PRIOR PILING DATE: 2001-06-21

PRIOR APPLICATION NUMBER: US 06/213,963

PRIOR APPLICATION NUMBER: US 06/213,963

PRIOR PILING DATE: 2000-06-23

PRIOR PILING DATE: 2000-06-23

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PRIOR PILING DATE: 2000-06-21

PRIOR PILING DATE: 2000-06-21
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Publication No. US20030096305A1
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887 CCAGGCAAAAACCAGAAGTTGACCAGAGTTGTAATCTACACGAAAGGCTGTGTGCGCCC 946
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      707 TAGACTTCACCCAGGAATATTGGCAGTGCTGTGGGGCTTTTGGAGCTGATGATTGGAACC
                                                               TTGACTTTGCTCAGGAATATTGGTCTTGCTGCGGAGCCCGAGGGCCTAATGACTGGAACC
                                                                                                                                            615 TCAATATCTATTTCAACTGCACTGACTTGAACCCGAGCCGAGGGGGCTGCGGGGTGCCCT
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Best Local Similarity 73.2%; Pred. No. 4.7e-118;
Matches 581; Conservative 0; Mismatches 209; Indels 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 205, Application US/09925299
Fublication No. US20030040617A9
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT APPLICATION NUMBER: C01-08-10
FRIOM FILING DATE: 2000-03-08
PRIOM FILING DATE: 2000-03-08
PRIOM FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: Patentin Ver. 2.0
FUNDATION OF SEC 10 NOS: 1556
SEQ ID NOS: 1556
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LOCATION: (1548)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (1559)
OTHER INFORMATION: n equals a,t,g, or c
LOCATION: (1564)
OTHER INFORMATION: n equals a,t,g, or c
LOCATION: (1564)
OTHER INFORMATION: n equals a,t,g, or c
LOCATION: (1626)
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US-09-925-299-205
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                                                                                                                                                                                                         APPLICANT: ROSen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REPERENCE: PAA02
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR PILING DATE: 2000-03-08
PRIOR PILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: PatentIn Ver: 2.0
SEQ ID NO 205
LENGTH: 1655
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17.4%; Score 441.6; DB 9;
Best Local Similarity 73.2%; Pred. No. 4.7e-118;
Matches 581; Conservative 0; Mismatches 209;
                                            NAME/KEY: misc feature
LOCATION: (1548)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (1559)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (1564)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (1623)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (1643)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (1643)
                  895 AGTGACATCAAGGCAGTGAAGGCCAACTGG
                                                                                                                                                     Sequence 205, Application US/09925299 Patent No. US20020055627A1 GENERAL INFORMATION:
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Pred. No. 2.1e-111;
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PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/149,447
PRIOR FILING DATE: 1999-08-18
PRIOR APPLICATION NUMBER: 60/138,573
PRIOR APPLICATION NUMBER: 60/137,797
PRIOR APPLICATION NUMBER: 60/137,797
PRIOR PLING DATE: 1999-06-03
PRIOR FILING DATE: 1999-05-19
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver: 2.0
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ORGANISM: Homo sapiens
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                                                        Sequence 5, Application US/10103196
Publication No. US20030050466A1
GENERAL INFORMATION:
GENERAL THORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: TM4SF POlynucleotides, Polypeptides, and Antibodies
FILE REFERENCE: PT008B1
CURRENT APPLICATION NUMBER: US/10/103,196
CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 09/707,936
PRIOR PILING DATE: 2000-01-08
PRIOR APPLICATION NUMBER: PCT/US00/13504
PRIOR PILING DATE: 2000-05-18
PRIOR PILING DATE: 2000-05-18
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APPLICANT: MCCON, JOHN M.
APPLICANT: Colling-Racie, Lisa A.
APPLICANT: Evans, Cheryl
APPLICANT: Evans, Cheryl
APPLICANT: Merberg, David
APPLICANT: Teacy, Maurice
APPLICANT: Steininger II, Robert J.
APPLICANT: Steininger II, Robert J.
APPLICANT: Spaulding, Vikki
APPLICANT: Spaulding, Vikki
APPLICANT: Spaulding, Vikki
APPLICANT: Wong, Gordon G.
APPLICANT: Resnick, Richard J.
APPLICANT: Resnick, Richard J.
APPLICANT: Resnick, Richard J.
APPLICANT: Genetics Institute, Inc.
APPLICANT: Genetics Institute, Inc
612 ACCTCAATATCTATTTCAACTGCACTGACTTGAACCCGAGCCGAGAGGCGCTGCGGGGTGC
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SENERAL INFORMATION:
RAPLICANT: Jacobs, Kenneth
APPLICANT: MCOY, John M.;
APPLICANT: LaVallie, Edward R.
APPLICANT: Collins-Racie, Lisa A.
APPLICANT: Collins-Racie, Lisa A.
APPLICANT: Applicant Grand
APPLICANT: Stand Grand
APPLICANT: Stand
APPLICANT: Treacy, Maurice
"LICANT: Steininger II, Robert J.
CANT: Bowman, Michael R.
"ICANT: Spaulding, Vikki
NT: Wong, Gordon G.
T. Clark, Hilary
T. Clark, Hilary
T. Fechtel, Kim
Howes, S.
Rep.
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US-10-103-196-10
i Sequence 10, Application US/10103196
i Publication No. US20030050466A1
i GENERAL INFORMATION:
i APPLICANTON TO US20030050466A1
i TITLE OF INVENTION: THASF POLYMUCLEOLIDES, POLYPEPLICANTON THASF POLYMUCLEOLIDES, POLYPEPLICANTON WINDER: US/10/103,196
i CURRENT APPLICATION NUMBER: US/10/103,196
i PRIOR APPLICATION NUMBER: US/10/103,196
i PRIOR FILING DATE: 2000-01-08
i PRIOR PLILING DATE: 2000-05-18
i PRIOR APPLICATION NUMBER: 60/178,770
i PRIOR PLILING DATE: 1999-06-18
i PRIOR PLILING DATE: 1999-06-11
i PRIOR FILING DATE: 1999-06-11
i PRIOR FILING DATE: 1999-05-19
i NUMBER: 60/135,122
i PRIOR FILING DATE: 1999-05-19
i NUMBER: PATENTIN NUMBER: 60/135,122
i PRIOR FILING DATE: 1999-05-19
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i PRIOR FILING DATE: 1999-05-19
i NUMBER: PATENTIN NUMBER: E0/135,122
i PRIOR FILING DATE: 1999-05-19
i NUMBER: PATENTIN NUMBER: E0/135,122
i PRIOR FILING DATE: 1999-05-19
i NUMBER: PATENTIN NUMBER: FULLING DATE: 1999-05-19
i LENGTH: 1178
i TYPE: DANA
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  CAGITIGAGAAGIGGCIGCAGGACAACCIGAICGIGGIGGCIGGGGTCIITGIGGGCAIC 849
                             135 AGCACTTCCAGGAACCCGAGGTCGGCTGCTGCGGGAAATACTTCCTGTTTGGCTTCAACA 194
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; ORGANISM: Homo sapiens
US-10-103-196-10
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Matches 564; Conservative
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                    LOCATION: (28)
OTHER INCORMATION: n
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                                                                        2 TGGAATGAAAAGGAGTTCTGTCCAACATCTCTTCCATCACCGATCTCGGCGCGCTTTGAC
                                                                                                                                                              62 CCAGTITIGECTCTTCCTIGIGEGAGGAGGAGTGTTCTTTTTGGATTTTGCAGGTGC
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                                         245 TGGGGTGAGAAGGGTGTTCTCTCCAACATCTGGGGTGACCGATCTGGGAGGCCTCGAC
                                                                                                                                  305 CCTGTGTGGCTGTTTGTAGTGGTTGGAGGCGTCATGTCCGTGCTGGGCTTTGCCGGCTGC
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    Gaps
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GENERAL INFORMATION:
APPLICANT: Ruben et. al.
TITLE OF INVENTION: 97 Human secreted proteins
FILE OF INVENTION: 97 Human secreted proteins
CURRENT FILING DATE: 2001-06-28
FRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-11-10
NUMBER OF SEQ ID NOS: 461
SOFTWARE: PARENTIN Ver. 2.0
SSOFTWARE: PARENTIN Ver. 2.0
LENGTH: 2672
    4
    Indels
Mismatches 172;
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FEATURE:
NAME/KEY: SITE
LOCATION: (16)
OTHER INFORMATION: n equals a,t,g, or
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Publication No. US20030077809A1
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Conservative
Matches 508;
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US-09-892-877-20
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AAGGACGCTGATCTCAGACATCGAGGCAGTGAAGGCC 975
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APPLICANT: Ruben et. 31.

TITLE OF INVENTION: 97 Human secreted proteins
TITLE OF INVENTION: 97 Human secreted proteins
TITLE REFERENCE: PEO208P2
CURRENT APPLICATION NUMBER: US/09/948, 783
CURRENT FILING DATE: 2001-09-10
FRIOR APPLICATION NUMBER: 09/892, 877
FRIOR APPLICATION NUMBER: 09/892, 877
FRIOR APPLICATION NUMBER: 09/892, 877
FRIOR APPLICATION NUMBER: 09/892, 877
FRIOR APPLICATION NUMBER: ED/085, 093
FRIOR APPLICATION NUMBER: 60/085, 094
FRIOR FILING DATE: 1998-05-12
FRIOR APPLICATION NUMBER: 60/085, 094
FRIOR FILING DATE: 1998-05-12
FRIOR APPLICATION NUMBER: 60/085, 105
FRIOR APPLICATION NUMBER: 60/085, 906
FRIOR PILING DATE: 1998-05-12
FRIOR APPLICATION NUMBER: 60/085, 906
FRIOR FILING DATE: 1998-05-18
FRIOR APPLICATION NUMBER: 60/085, 921
FRIOR FILING DATE: 1998-05-18
FRIOR APPLICATION NUMBER: 60/085, 921
FRIOR APPLICATION NUMBER: 60/085, 921
FRIOR APPLICATION NUMBER: 60/085, 921
FRIOR APPLICATION NUMBER: 60/085, 922
FRIOR FILING DATE: 1998-05-18
FRIOR FILING DATE: 1998-05-18
FRIOR FILING DATE: 1998-05-18
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FRIOR FILING DATE: 1998-05-18
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                                                                                                                                                                                                                             Sequence 20, Application US/09948783
Publication No. US20030100051A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
FEATURE:
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NAME/KEY: SITE
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OTHER INFORMATION:
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; OTHER INFORMATION:
US-09-948-783-20
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                                                                                                                                                                                                                                                                                                                279 TGGAGTCGGGCTGTGGGCATGGAGGGAAAAGGGTGTGCTGTCCGACCTCACCAAAGTGAC 338
                                                                                                                                                                                                                                                                                                                                                                                            286 CGATCTGGGAGGCCTCGACCCTGTGTGGCTTGTAGTGGTTGGAGGCGTCATGTCCGT 345
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                                          Gaps
    2672;
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9
    Length
  Score 357.4; DB 11; Length
Pred. No. 2.5e-93;
3; Mismatches 304; Indels
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Publication No. US20030027998A1
GENERAL INFORMATION:
APPLICANT: McCarthy, Sean A.
ITILE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                882 CCAGAACCTTGTGAGTGACATCAAGGCAGTGAAGGCC 918
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  Query Match
Best Local Similarity 64.3%;
Matches 564; Conservative
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US-09-796-753-125
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DB 11; Length 2715;
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13.9%; Score 353.4; DB 11; Length
Best Local Similarity 67.0%; Pred. No. 3.7e-92;
Matches 518; Conservative 0; Mismatches 251; Indels
PRICE REPRENCE: 7853-227-959

CURRENT APPLICATION NUMBER: 09/183,175

PRIOR APPLICATION NUMBER: 09/223,094

PRIOR FILING DATE: 1998-10-30

PRIOR FILING DATE: 1998-12-30

PRIOR FILING DATE: 1999-12-30

PRIOR FILING DATE: 1999-12-30

PRIOR FILING DATE: 1999-02-26

PRIOR FILING DATE: 1999-02-26

PRIOR FILING DATE: 1999-02-26

PRIOR FILING DATE: 1999-02-26

PRIOR FILING DATE: 1999-02-30

PRIOR PRILING DATE: 1999-02-30

PRIOR PRILING DATE: 1999-06-14

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PRIOR PRILING DATE: 1999-07-30

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US-09-796-753-125
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                                                                                                 390 TCCTGCTCAAGTTTTTCTCAGTGTTCCTTGGCCTCATCTTCTTCCTGGAGCTGGCAACAG
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Search completed: November 21, 2003, 21:46:20 Job time : 774 secs

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ORGANISM: Homo sapiens
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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               GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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US-08-855-140-4
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US-09-020-956-114

US-09-330-607-114

US-09-323-1144

US-09-322-149A-114

US-09-149-76-429

US-09-149-76-429

US-08-957-130-13

US-08-957-130-13

US-08-957-130-13

US-08-957-130-13

US-08-952-21-443

US-08-952-8198

US-08-328-352-8198

US-09-731-030A-11

US-09-731-030A-13

US-09-328-352-7457

US-09-328-352-7457

US-09-133-347-5

US-08-133-347-5
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Patent No. 6534631
GRERAL INFORMATION
GRERAL INFORMATION
TITLE OF INVENTION: 71 Human Secreted Proteins
TITLE OF INVENTION: 71 Human Secreted Proteins
TITLE OF INVENTION: 71 Human Secreted Proteins
CURRENT APPLICATION NUMBER: US/09/482,273
CURRENT FILING DATE: 2000-01-13
FARLIER FILING DATE: 1999-07-15
EARLIER PILING DATE: 1999-07-15
EARLIER PILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
SOFTWARE: PILING DATE: 1998-07-15
NUMBER: OF SEQ ID NOS: 267
SOFTWARE: PARITH VOR: 2.0
SEQ ID NO 133
LENGTH: 285
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; OTHER INFORMATION: Xaa equals stop translation
US-09-482-273-133
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Onrust, Rene

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            Jeguence 181, Application US/09188930A

General No. 6150502

GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Stream, Matthew
APPLICANT: Steeman, Matthew
APPLICANT: Orrust, Rene
APPLICANT: Orrust, Rene
APPLICANT: Orrust, Rene
APPLICANT: Murison, James Greg
ITTLE OF INVENTION: Compositions Isolated From Skin Cells
ITTLE OF INVENTION: and Methods For Their Use
ITTLE OF INVENTION: and Methods For Their Use
ITTLE OF INVENTION: NUMBER: US/09/188,930A

CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 60

ILENGTH: 60

TYPE: PRT

CORGANISM: mouse
US-09-188-930-181
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APPLICANT Strachan, Lorna
APPLICANT Strachan, Lorna
APPLICANT Steeman, Matthew
APPLICANT Onrust, Rene
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT PILIOG DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20.7%; Score 265; DB 3; Length 60;
nilarity 75.9%; Pred. No. 3.1e-22;
Conservative 6; Mismatches 8; Indels
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75.9%; Pred. No. 3.1e-22;
tive 6; Mismatches 8;
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US-09-188-930-320
Sequence 320, Application US/09188930A
Perent No. 6150502
GENERAL INFORMATION:
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Patent No. 6573095

GENERAL INFORMATION:

APPLICANT: Watson, James D.

APPLICANT: Strachan, Lorna

APPLICANT: Sleeman, Matthew
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Matches 44; Conserva
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Best Local Similarity
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; ORGANISM: Mouse
US-09-188-930-320
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US-09-188-930-181
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Patent No. 624598
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Testa, Jacqueline E.
APPLICANT: Quigley, James P.
APPLICANT: Seandel, Marco
TITLE OF INVENTION: MONOCLAND WITH TUMOR METASTASIS
FILE REFERENCE: SUNY
CURRENT PAPLICATION NUMBER: US/09/333,599
CURRENT FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 2.0
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Munison, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated from Skin Cells
TITLE OF INVENTION: and Methods for Their Use
FILE REFERENCE: 11000.1011c2
CURRENT APPLICATION NUMBER: US/09/312,283C
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 425
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 320
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 265; DB 4; Length 60;
Pred. No. 3.1e-22;
6; Mismatches 8; Indels
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APPLICANT: Murison, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated from Skin Cells
TITLE OF INVENTION: Compositions Isolated from Skin Cells
TITLE OF INVENTION: and Methods for Their Use
PILE REFERENCE: 11000.1011c2
CURRENT APPLICATION NUMBER: US/09/312,283C
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ. ID NOS: 425
SOFTWARE: PASLEEQ for Windows Version 4.0
SEQ. ID NO. 181
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20.7%; Score 265; DB 4;
Best Local Similarity 75.9%; Pred. No. 3.1e-22;
Matches 44; Conservative 6; Mismatches 8;
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Best Local Similarity 75.94
Matches 44; Conservative
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US-09-312-283C-181
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ORGANISM: Mouse
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US-08-855-140-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 YILVVAGVVVMVTGVLGCCATFKERRNLLRLYFILLLIFLLEIIAGILAYVYQQLLNTE 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFFINNN-VKAYRDD--IDLQNLIDFAQEYWSCCGARGPNDWNLNIYFNCTDLNPSRER 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 FOEPEVGC---CGKYFLFGFNIVFWVLGALFLAIGLWAWGEKGVLSNISALTDLGGLDPV 64
                                                                                                                                                                                                                                                                                                                                                                8 FQEPEVGC---CGKYFLFGFNIVFWVLGALFLAIGLWAWGEKGVLSNISALTDLGGLDPV 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/09499781
| Sequence 4, Application US/09499781
| Patent No. 6498014
| GENERAL INFORMATION:
| APPLICANT: Testa, Jaqueline E. APPLICANT: Quigley, James P. APPLICANT: Seandel, Marco
| TITLE OF INVENTION: MONOCLONAL ANTIBOIDES THAT RECOGNIZE ANTIGENS | TITLE OF INVENTION: MONOCLONAL ANTIBOIDES THAT RECOGNIZE ANTIGENS | TITLE OF INVENTION: MONOCLONAL ANTIBOIDES THAT RECOGNIZE ANTIGENS | FILE REFERENCE: SUNY | CURRENT APPLICATION NUMBER: US/09499,781 | CURRENT FILING DATE: 1999-06-15 | PRIOR APPLICATION NUMBER: 09/333,599 | PRIOR PILING DATE: 1999-06-15 | SOFTWARE: Patentin Ver. 2.0 | SOFTWARE: Patentin Ver. 2.0 | SOFTWARE: Patentin Ver. 2.0 | SOFTWARE: Patentin Ver. 2.0 | SOFTWARE: Patentin Ver. 2.0 | SOFTWARE: Patentin Ver. 2.0 | SOFTWARE: Patentin Ver. 2.0 | SOFTWARE: Patentin Ver. 2.0 | SOFTWARE: Patentin Ver. 2.0 | SOFTWARE: Patentin Ver. 2.0 | SOFTWARE: Patentin Ver. 2.0 | SOFTWARE: Patentin Ver. 2.0 | SOFTWARE: Patentin Ver. 2.0 | SOFTWARE: Patentin Ver. 2.0 | SOFTWARE: Patentin Ver. 2.0 | SOFTWARE: Patentin Ver. 2.0 | SOFTWARE: Patentin Ver. 2.0 | SOFTWARE: Patentin Ver. 2.0 | SOFTWARE: Patentin Ver. 2.0 | SOFTWARE: Patentin Ver. 2.0 | SOFTWARE: Patentin Ver. 2.0 | SOFTWARE: Patentin Ver. 2.0 | SOFTWARE: Patentin Ver. 2.0 | SOFTWARE: Patentin Ver. 2.0 | SOFTWARE: Patentin Ver. 2.0 | SOFTWARE: Patentin Ver. 2.0 | SOFTWARE: Patentin Ver. 2.0 | SOFTWARE: Patentin Ver. 2.0 | SOFTWARE: Patentin Ver. 2.0 | SOFTWARE: Patentin Ver. 2.0 | SOFTWARE: Patentin Ver. 2.0 | SOFTWARE: Patentin Ver. 2.0 | SOFTWARE: Patentin Ver. 2.0 | SOFTWARE: Patentin Ver. 2.0 | SOFTWARE: Patentin Ver. 2.0 | SOFTWARE: Patentin Ver. 2.0 | SOFTWARE: Patentin Ver. 2.0 | SOFTWARE: Patentin Ver. 2.0 | SOFTWARE: Patentin Ver. 2.0 | SOFTWARE: Patentin Ver. 2.0 | SOFTWARE: Patentin Ver. 2.0 | SOFTWARE: Patentin Ver. 2.0 | SOFTWARE: Patentin Ver. 2.0 | SOFTWARE: Patentin Ver. 2.0 | SOFTWARE: Patentin Ver. 2.0 | SOFTWARE: Patentin Ver. 2.0 | SOFTWARE: Patentin Ver. 2.0 | SOFTWARE: Patentin Ver. 2.0 | SOFTWARE: Patentin Ver.
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                                                                                                                                                                                               Length 253;
                                                                                                                                                                                         Ouery Match 18.7%; Score 240; DB 3; Best Local Similarity 31.4%; Pred. No. 1.4e-18; Matches 59; Conservative 32; Mismatches 85.
                                                             ; TYPE: PRT
; ORGANISM: Mus musculus
US-09-333-599-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182 CGVPFSCC 189
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ORGANISM: Mus musculus
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Best Local Similarity
Matches 59; Conserv
SEQ ID NO 4
LENGTH: 253
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RESULT 8 US-08-855-140-4

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75 SVLGFAGCIGALRENTFLLKFFSVFLGLIFFLELATGILAFVFKDWIRDQLNFFINNNVK 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         135 AYRDDIDLQNLIDFAQEYWSCCGARGPNDWNLNIYFNCTDLNPSRERCGVPFSCCVRDPA 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18.6%; Score 239; DB 2; Length 219; 30.9%; Pred. No. 1.4e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72; Indels
Sequence 4, Application US/08855140
Patent No. 5854022
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Karl J.
TITLE OF INVENTION: New TRANSMEMBRANE PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDERS ADDRESS:
ADDRESSEE: ADDRESSEE:
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/855,140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: BAllings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 30.22.
Thea 63; Conservative
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                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
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CLONE: 1279546
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IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                             USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 KYLMFAFNLLFWLGGGGVLGVGIWLAAQQGSFATLSS----SFPSLWAANLLIITGAFV 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 18.4%; Score 236.5; DB 3; Length 236;
1 Similarity 28.9%; Pred. No. 3e-18;
56; Conservative 34; Mismatches 83; Indels 21;
APPLICANT: Paul Moore, Reiner Gentz, Hongjin Ji,
APPLICANT: Jian Ni and Jing-Shan Hu
TITLE OF INVENTION: Human Genes, Sequences and
TITLE OF INVENTION: Expression Products
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CRECHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
STREET: NEW JERSEY
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08855140
Patent No. 5854022
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NEW TRANSMEMBRANE PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       325800-346 (PF196)
                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/705,771
FILING DATE: AUGUST 30, 1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
                                                                                                                                                                                                                                                   ZIP: 07068
COMPOTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 32:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 973-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 973-994-1/44
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acids
TOPOLOGY: lin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193 PAMSSTPSVAMMSG 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-08-705-771-19
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Best Local Similarity
Matches 56; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Palo Alto
                                                                                                                                                                                                                             COUNTRY: US
ZIP: 07068
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US-08-855-140-3
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75 SVLGFAGCIGALRENTFILKFFSVFLGLIFFLELATGILAFVFKDWIRDQLNFFINNNVK 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 KYFLFGFNIVFWVLGALFLAIGLW--AWGEKGVL-SNISALTDLGGLDPVWLFVVVGGVM 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 KYVLFFFNLLFWICGCCILGFGIYLLIHNNFGVLFHNLPSLT-LGN-----VFVIVGSII 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       135 AYRDDIDLONLIDFAQEYWSCCGARGPNDWNLNIYFNCTDLNPSRERCGVPFSC 188
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US-08-807-044-3
; Sequence 3, Application US/08807044
; Setent No. 5863735
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN TRANSMEMBRANE 4 SUPERFAMILY
NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
; STREET: ADD Alto
; STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64; Indels
          COMPUTER PASSABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: DISKETTE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
ATTORNEY, AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
TELEBRONE: 415-855-0555
TELEBRONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match

18.4%; Score 235.5; DB 2
Best Local Similarity 31.0%; Pred. No. 3.5e-18;
Matches 54; Conservative 31; Mismatches 64
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SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 RYHSDNSTKAAWDSIQSFLQCCGINGTSDWT--
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 219 amino acida
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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94304
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US-09-333-599-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 KYFLFGFNIVFWVLGALFLAIGLW--AWGEKGVL-SNISALTDLGGLDPVWLFVVVGGVM 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           135 AYRDDIDLONLIDFAQEYWSCCGARGPNDWNLNIYFNCTDLNPSRERCGVPFSC 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----SGPPASC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION. Rapid Immunoselection Cloning Method NUMBER OF INVENTION: Rapid Immunoselection Cloning Method CORRESPONDENCES: 2
ADDRESSEE: Greenles
STREEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 18.4%; Score 235.5; DB 2; Length Best Local Similarity 31.0%; Pred. No. 3.5e-18; Matches 54; Conservative 31; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
GOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNDER: PCT/US91/04986
FILING DATE: 19910715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 RYHSDNSTKAAWDSIQSFLQCCGINGTSDWT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3: Greenlee & Associates
5370 Manhattan Circle, Suite 201
                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0224 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
APPLICATION NUMBER: US/08/807,044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application PC/TUS9104986 GENERAL INFORMATION:
                                                                                                                                                                                                                              TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 219 amino acids
TYPE: amino acid
STRANDEDMESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seed, Brian
Allen, Janet
Aruffo, Alejandro
Camerini, David
Lauffer, Leander
Oquendo, Carmen
Simmons, David L.
             FILING DATE: Herewith CLASSIFICATION: 530 PRIOR APPLICATION DATA: APPLICATION NUMBER: FILING DATE:
                 Herewith
                                                                                                                                                                                                                                                                                                                                                                                  LIBRARY: GenBank
CLONE: 180141
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STATE: Colorado
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                               IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-807-044-3
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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10 KYVLFFFNLLFWICGCCILGFGIYLLIHNNPGVLFHNLPSLT-LGN-----VFVIVGSII 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 KYFLFGFNIVFWVLGALFLAIGLM--AWGEKGVL-SNISALTDLGGLDPVWLFVVVGGVM 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64
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18.2%; Score 234; DB 3; Length 253;
Best Local Similarity 31.0%; Pred. No. 6.3e-18;
Matches 61; Conservative 29; Mismatches 77; Indels 30; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09333599;
Patent No. 6245898;
GENERAL INFORMATION:
APPLICANT: Clasta, James P.
APPLICANT: Guigley, James P.
APPLICANT: Guigley, James P.
TITLE OF INVENTION: MONOCLONAL ANTIBOIDES THAT RECOGNIZE ANTIGENS;
TITLE OF INVENTION: MONOCLONAL ANTIBOIDES THAT RECOGNIZE ANTIGENS;
TITLE OF INVENTION: MONOCLONAL ANTIBOIDES THAT RECOGNIZE ANTIGENS;
TITLE REPERENCE: SUNY
CURRENT APPLICATION NUMBER: US/09/333,599
CURRENT FILIA DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         135 AYRDDIDLQNLIDFAQEYWSCCGARGPNDWNLNIYFNCTDLNPSRERCGVPFSC 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------SGPPASC 161
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/553,759
FILING DATE: 13-JUL-1990
PRIOR APPLICATION NUMBER: US 07/498,809
FILING DATE: 23-WAR-1990
PRIOR APPLICATION NUMBER: US 07/379,076
FILING DATE: 13-JUL-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/160,416
FILING DATE: 25-FEB-1988
ATTOMING DATE: 25-FEB-1988
ATTOMING DATE: 18-1988
ATTOMING DATE: 18-1988
ATTOMING DATE: 18-1988
ATTOMING DATE: 18-1988
ATTOMING DATE: 19-1988
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 303-499-8089
TELEFAX: 303-499-8089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 303-499-802,
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 219 amino acids
TYPE: AMINO ACID
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PCT-US91-04986-2
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                                       WLFVVVGGVMSVLGFAGCIGALRENTFLLKFFSVFLGLIFFLELATGILAFVFKDWIRDQ 124
                                                                                                                                                  LNFFINNNVKAYRDDID-------LQNLIDFAQEYWSCCGARGPNDWNLNIYFNCTD 174
                                                                                                                                                                                                 62 YILVVAGTVVWVTGVLGCCATFKERRNILRLYFILLLIIFLLEIIAGILAYAY----YQQ 117
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CURRENT FILING DATE: 2000-02-08
PRIOR FILING DATE: 1999-06-15
MINDER OF SUNG TEERS OF SUNGERIAL SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS OF SUNG TEERS 
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Patent No. 5854022
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NEW TRANSMEMBRANE PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09499781
Patent No. 6498014
                                                                                                                                                                                                                                                                                                    175 LNPSRERCG--VPFSCC 189
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CRGANISM: Homo sapiens
US-09-499-781-2
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Best Local Similarity
Matches 61; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Pat
SEQ ID NO 2
LENGTH: 253
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US-09-499-781-2
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US-08-855-140-1
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CITY: Palo Alto

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75 SVLGFAGCIGALRENTFLLKFFSVFLGLIFFLELATGILAFVFFDWIRDQLNFFINNNVK 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 LYHTENNVGLKNAWNIIQAEMRCCGVTDYTDW------YPVLGENTVPDRCCM-- 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 CCLKYMMFLFNLIFWLCGCGLLGVGIWLSVSQGNFATFS--PSFPSLSAANLVIAIGTIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 CCGKYFLFGFNIVFWVLGALFLAIGLWAWGEKGVLSNISALTDLGGLDPVWLFVVVGGVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18.1%; Score 232; DB 2; Length 280; ilarity 27.5%; Pred. No. 1.2e-17; Conservative 30; Mismatches 92; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  193 PAMSSTPSVAMMSGSNWSWSSRAPYTPKAVWASLRSGC 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------ENSQGCGRNGTIP--LW---RTGC 190
                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: DOS
SOFRATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/855,140
                                                                                                                                                                                                                                                                                   APPLIANT
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0296 US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 completed: November 21, 2003, 13:46:00 le : 22 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 280 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                     FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MYOMNOT01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 60; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIBRARY: MYOMI
CLONE: 779308
94304
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November 21, 2003, 13:41:03 ; Search time 35 Seconds (without alignments) 1717.893 Million cell updates/sec
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1283
1 MPGKHQHFQEPEVGCCGKYF......RAPYTPKAVWASLRSGCRTT 233
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                    OM protein - protein search, using sw model
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sp_bacteria:*
sp_human:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		Description	O96fv3 homo gaptien		87111	mus	E I	Pomod		C III	D D D	drogo		Ogeage Cand					
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Result

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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MEDLINE=2108566; PubMed=11217851;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC010346; AAH10346.1; -.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DBC-2003 (TrEMBLrel. 23, Last annotation update)
RIKEN COMA 2210021G21 gene.
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InterPro; IPR000301; Transmem 4.
Pfam; PF00315; transmembrane4; 1.
PRINTS; PR00259; TMFOUR.
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01-JUN-2001 (TrEMBLrel. 17, La
01-JUN-2001 (TrEMBLrel. 17, La
2210021G21Rik protein.
2210021G21RIK.
Mug musculus (Mouse).
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RCGVPFSCCVRDPA 194
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TISSUE=Breast tumor;
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61 LDPVWLFVVVGGVMSVLGFAGCIGALRENTFLLKFFSVFLGLIFFLELATGILAFVFKDW 120
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Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suurki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Frunno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Garibodi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamibadi M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.F., Suzuki H., Toyo-Oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshwa-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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TM4SF9 OR 2810455A09RIK.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17, Last sequ
01-CCT-2002 (TrEMBLrel. 22, Last anno
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EMBL; AK008/61; BAB25880 1; -
MGD; MGI-1921507; 2210021G21Rik.
InterPro; IRR00301; Transmem_4.
Pfam; PF00335; transmembrane4; 1.
PRINTS; PR00259; TWFOUR.
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Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y.; Functional annotation of a full-length mouse cDNA collection."; Functional annotation of a full-length mouse cDNA collection."; EMBL; AKO1336; BAR28804.]; -. EMBL; AKO1336; TM48f9.

InterPro; IRRO0301; Transmem 4.
Pfam: PP00315; transmembrane4; 1.
Pfam: PP00315; transmembrane4; 1.
PRINTS; PR0025; TMFOUR.
SEQUENCE 266 AA; 30040 MW; ASOOCFA6192D091D CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to region containing hypothetical protein MGC11352, slingshot (Hypothetical protein) (Similar to transmembrane 4 superfamily member
                                                                                                                                                                                                             Gaps
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"Analysis of the mouse transcriptome based on functional annotation
60,770 full-length cDNAs.";
Nature 420:563-573 (2002)
Wature 420:563-573 (2002)
EMBL; BC024611; AAH24611.1; -.
EMBL; BC025568; AAH25568.1; -.
EMBL; BC026574; AAH26574.1; -.
EMBL; BC026574; AAH26574.1; -.
EMBL; MC036593; BAC27035.1; --
MGD; MGI:1196325; D14Ertd226e.
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D14ERTD226E OR AA958793.
Buks musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; MuslaraxID=10090;
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                                                                                                                                                                              Query Match 69.0%; Score 885; DB 11; Length 266; Best Local Similarity 79.9%; Pred. No. 1.4e-67; Matches 155; Conservative 16; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases
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TISSUE=Salivary gland;
Strausberg R.;
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65 WLFVVVGGVMSVLGFAGCIGALRENTFLLKFFSVFLGLIFFLELATGILAFVFKDWIRDQ 124
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                          Query Match 50.4%; Score 646.5; DB 11; Length 270; Best Local Similarity 50.6%; Pred. No. 2.9e-47; Matches 122; Conservative 34; Mismatches 66; Indels 19;
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Zhang W., il. N., Wan T., Cao X.;
"Idencification of novel membrane proteins ";
"Unitred (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF311293, AAM94899.1; -
InterPro; IPR00301; Transmem_4.
PRINTS; PR00259; TMFOUR.
SEQUENCE 270 AA, 30691 WW, C74D64CDC52DP107 CRC64;
InterPro, IPR000301; Transmem_4.
Pfam; PF00335; transmembrane4; 1.
Hypothetical protein.
SEQUENCE 270 AA; 30674 MW; 814DF8AF38E360CB CRC64;
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Last annotation update)
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36;

RESULT 7

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106 FREFFESNIKSYRDDIDLQNLIDSLQKANQCCGAYGPEDWDLNVYFNCSGASYSREKCGV 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LNFFINNNVKAYRDDIDLQNLIDFAQEYWSCCGARGPNDWNLNIYFNCTDLNPSRERCGV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFSCCVRDPAMSSTPS----VAMMSGSNW-----SWSSRAPYTPKAVWAS 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          166 PFSCCVPDPAQKVVNTQCGYDVRIQLKSKWDESIFTKGCIQALESWLPRNIYIVAGVFIA 225
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                                                                                                                                                                                                                                                                                                                                                        3 YYRYSNAKVSCWYKYLLFSYNIIFW---------GVLSDLTKVTRMGIDPV
                                                                                                                                                                                                                                                                                                                                5 HQHFQEPEVGCCGKYFLFGFNIVFWVLGALFLAIGLWAWGEKGVLSNISALTDLGGLDPV
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-20003060; PubMed-10531035;
Cenciarelli C., Chiaur D.S., Guardavaccaro D., Parks W., Vidal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38.0%; Score 487.5; DB 4; Length 123; 85.0%; Pred. No. 4.3e-34; tive 1; Mismatches 11; Indels 5.
                                                                                                                                                                                                                                              43.2%; Score 554; DB 4; Length 253; 45.2%; Pred. No. 2e-39;
                                                                                                                                                                                                                                                                                       Indels
                                                            Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC002920; AAH02920.1; -.
InterPro; IFR00301; Transmem 4.
Pfam; PP00315; transmembrane4; 1.
PRINTS; PR00259; TMFOUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pagano M.;
"Identification of a family of human F-box proteins.";
"Identification of a family of human F-box proteins.";
Curr. Biol. 9:1177-1179 (1999).
EMBL; AF74601; AAF04524.1; -.
Genew; HGNC.13594; FBXO23.
InterPro; IPR000301; Transmem_4.
Pfan; PF00335; transmembrane4; 1.
                                                                                                                                                                                                        253 AA; 28876 MW; F83140442CFCAC16 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 123
123 AA; 13531 MW; OA6CDB2AF450DBEF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
F-box protein Fbx23 (Fragment).
                                                                                                                                                                                                                                                                                         62;
                                                                                                                                                                                                                                                                  45.2%; Pred. No. 2e-3
tive 34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 AA
                                                                                                                                                                                                                                                                      Best Local Similarity 35.2.1
Matches 109; Conservative
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hes 96; Conservative
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                                                                                                                                                                                                                                                                    Similarity
[1]
SEQUENCE FROM N.A.
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                                                                                                                                                                                      Transmembrane
                                           TISSUE=Skin;
                                                                                                                                                                                                          SEQUENCE
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SEQUENCE
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Q9UKB9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 FREFFESNIKSYRDDIDLQNVIDSLQKANQCCGAYGPEDWDLNVYFNCSGASYSREKCGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 HOHFOEPEVGCCGKYFLFGFNIVFWVLGALFLAIGLMAWGEKGVLSNISALTDLGGLDPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 LNFFINNNVKAYRDDIDLQNLIDFAQEYWSCCGARGPNDWNLNIYFNCTDLNPSRERCGV
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Similar to transmembrane 4 superfamily member 9.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21154917; PubMed=11230166; Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S., Miemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S., Blum H., Lauber J., Duesterhoeft A., Bloecker H., Schrer K., Strack N., Mewes H.W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D., Wambutt R., Korn B., Klein M., Poustka A.; "Towards a Catalog of Human Genes and Proteins: Sequencing and Analysis of 500 Novel Complete Protein Coding Human cDNAs."; Genome Res. 11:422-435(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
49.5%; Score 635.5; DB 4; Length 270;
Best Local Similarity 49.0%; Pred. No. 2.5e-46;
Matches 118; Conservative 38; Mismatches 66; Indels 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
SEQUENCE 270 AA; 30696 MW; 4558912DC5381108 CRC64;
                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                      270 AA
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                                                                                                                                                               Created)
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                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-OCT-2002 (TrEMBLrel. 22,
Hyporhetical protein.
                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE=Brain;
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243 I 243
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GGLDPVWLFVVVGGVMSVLGFAGCIGALRENTFLLKFFSVFLGLIFFLELATGILAFVFK 118 61 -ALDPAFVLIILGGVTFLLGFMGSVGALRENTCLLGAYAIFLSVLLIAEIGFCAVAFVLK 119 D--WIRDQLNFFINNNVKAYRDDIDLQNLIDFAQEYW-SCCGARGPNDWNLNIYFNCTDL 175 120 DKGWIKDQATEGLKAFIRHYREDADQQNLIDWIQEDWLQCCGIDGPKDWDSNNYFNCSSI 179

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RX ARTAMS=EBSTREEEN;
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RX ARAMS=EBSTREEEN;
RX SURTON G.C., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RX Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,
RX Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,
RX Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,
RX Ballew R.M., Basu A., Baxendale J., Bardario D., Bolahakov S.,
RX Beson K.Y. Benos P.V., Berma B.P., Bardario D., Bolahakov S.,
RX Beson K.Y. Benos P.V., Berma B.P., Brotteier P.,
RX Berkova D., Botcham M.R., Bouck J., Brokstein P., Brotteier P.,
RX Berkova D., Botcham M.R., Bouck J., Brokstein P., Brotteier P.,
RX Borkova D., Botcham M.R., Bouck J., Brokstein P., Brotteier P.,
RX Borkova D., Botcham A., Bullke C., Davenpoort L.B., Davies P.,
RX Botson K.J., Evangeliste C.C., Ferraz C., Ferriera S., Punkov B.C., Dunn P.,
RX Botson K.J., Evangeliste C.C., Ferraz C., Ferriera S., Punkov B.C.,
Durbin K.J., Evangeliste C.C., Ferraz C., Gelbart W.M., Glasser K.,
RY Gober C., Gabrielian A.E., Gabry N.S., Gelbart W.M., Glasser R.,
RY Goldek A., Gong F., Gorrell J.H., Gu Z., Gulbar P., Harris M.
Alalai M., Kalush F., Ratpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Alalai M., Kalush F., Ratpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Alalai M., Kalush F., Ratpen G.H., Ke Z., Kennison D.L.,
RN Hostin D., Housten K.A., Hown W. Mobarry C., Morris J., Moshrefi A.,
RN Hortin W., Murphy B., Murphy L., Murny D.M., Nelson D.L.,
RN Hoston D.R., Wolly W., Murphy B., Murphy L., Murny D.M., Nelson D.K.,
RN Hostin M., Falusos I., Simpson M., Stupski M.P., Shrad K.,
Spier E., Spradin-Klamos I., Simpson M., Stupski M.P.,
Spier E., Spradin-Klamos I., Simpson M., Stupski M., Wassenbach J.,
Walliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Zhu X., Smith H.O.,
RY Hostin W. Wyer B., Rubin G.W., Zhon S., Palland J.C.,
Shence 287, 22000, S.,
RY Hostin W., Warsenbach J., Wass
LDPVWLFVVVGGVMSVLGFAGC---IGALRENTFLLKFFSVFLGLIFFLELAT 110
                                    Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
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InterPro; IPR000301; Transmem 4.
Pfam; PF00335; transmembrane4; 1.
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TSP26A OR CG9093.
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63 PVWLFVVVGGVMSVLGFAGCIGALRENTFLLKFFSVFLGLIFFLELATGILAFVFKDWIR 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 DOLNFFINNNVKAYRDDIDLONLIDFAQEYWSCCGARGPNDWNLNIYFNCTDLNPSRERC 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 GKHQHFQEPEVGCCGKYFLFGFNIVFWVLGALFLAIGLWAWGEKGVLSNISALTDLGGLD 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 GDEFSFVSPLV----KYLLFFFNMLFWVISMYMVAVGVYARLMKJAEAALACL----AVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi; Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                  01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to transmembrane 4 superfamily member (Tetraspan NET-7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GVPFSCCVRDP -- AMSSTPSVAMMSGSNWSWSSRAPYTPKAVWASLRSGC 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              224
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 36.8%; Score 472.5; DB 11; Length 283; Best Local Similarity 43.5%; Pred. No. 1.9e-32; Matches 100; Conservative 41; Mismatches 70; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184 SVPYSCCEPTPNQAVINTMCGQGMQALDYLEASKVIYT-----NGC
                                                                                                                                                                                                                                                                        Strausberg R.; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC024685; AAH24685.1; -. InterPro; IPR000301; Transmem_4.
                                                                                                                                                                                                                                                                                                                                                                                           283 AA; 31550 MW; 9AF1515D5B0EF5CF CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UUN-2002 (TrEMBLrel. 21, Last annotation update)
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       283
                                        01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last seq
01-MAR-2003 (TrEMBLrel. 23, Last ann
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Zhang W., Li N., Wan T., Cao X.;
PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tetraspan protein SB134.
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                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                        Transmembrane
SEQUENCE 28
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  Q8R3S2
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65; Indels

35; Mismatches

46.2%;

92; Conservative

Similarity

Local

Matches

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10
                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                              Matches
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        SOR DREAT A SOR BRANCE SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DREAT A SOR DRE
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                                                                                                                                                                                                                                                                                                                                                                61 LDPVWLFVVVGGVMSVLGFAGCIGALRENTFLLKFFSVFLGLIFFLELATGILAFVFKDW 120
                                                                                                                                                                                                                                                            1 MPGKHQHFQEPEVGCCGKYFLFGFNIVFWVLGALFLAIGLWAWGEKGVLSNISALTDLGG 60
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Eukaryota, Metazoa; Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera; Endopterygota, Diptera, Brachycera; Muscomorpha, Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                             Length 188;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY037146; AAK67627.1; -.
InterPro; IPR000301; Transmem.
Pfam; PF00135; transmembrane4; 1.
SEQUENCE 188 AA; 21441 MW; D69DD8412129D029 CRC64;
                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                          Score 423; DB 4;
Pred. No. 2.1e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 IRDQLNFFINNNVKAYRDDIDLQNLIDFAQEY 152
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                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55 IRDQLNLFINNNVKAYRDDIDLQNLIDFAQEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                          33.0%;
55.9%;
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                                                                                                                                       Query Match
Best Local Similarity 55.9'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                      SEQUENCE
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  SORRES
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64 VW------LFVVVGGVMSVLGFAGCIGALRENTFLLKRFSVFLGLIFFLELATGILAF 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  173 TDLNPSRERCGVPFSCCVRDPAMSSTPSVAMMSGSNWSWSSRAPYTPKAVWASLRSGC 230
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н.о.,
                                                                                                                                                                                                                                                                                                                                                    7 HFQEPEVGCCGKYFLFGFNIVFWVLGALFLAIGLWAWGEKGVLSNISALTDLGG---LDP
                                                                                                                                                                                                                                                                                                                                                                                          23 HFS--YVSSCVKYMIFLLNFLFWLFGGLLLAIGVYAFMDK-----LMDGNGWLRLDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EPEVGCCGKYFLFGFNIVFWVLGALFLAIGLWAWGEKGVLSNISALTDLGGLDPVWLFVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng I Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith F Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                           31;
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                                                                                                                                                                                                                                                                   DB 5; Length 291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32.7%; Score 419.5; DB 5; Length 308; 42.9%; Pred. No. 6.9e-28; ive 32; Mismatches 71; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                          FlyBase; FBgn0037848; Tsp86D.
InterPro; IPR000301; Transmem 4.
Pfam; PF00315; transmembrane4; 1.
PRINTS; PR00259; TMFOUR.
SEQUENCE 291 AA; 33213 MW; ES7FC55688B65C3D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  308 AA; 34658 MW; E37221DDD2ADE78E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                         32.9%; Score 421.5; DB 5;
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MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 42.9%
tes 78; Conservative
                                                                                                                                                                                                                                                                                  Local Similarity 40.8 tes 97; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans.
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6
NNNVKAYRDDIDLQNLIDFAQEYWSCCGARGPNDWNLNIYFNCTDLN-PSRERCGVPFSC 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 GGLDPVWLFVVVGGVMSVLGFAGCIGALRENTFLLKFFSVFLGLIFFLELATGILAFVFK 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 DWIRDQL-NFINNNVKAYRDDIDLQNLIDFAQEYWSCCGA--RGPNDWNLNIYFNCTDL 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 VGCCGKYFLFGFNIVFWVLGALFLAIGLWAWGEK-------GVLSNISALTDL 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 VSQCVKYMIFLLNFVFWLFGGLLLGIGVYAFRDKWEDANGSVRLENFYDVFLNISLVMIL 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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TO 1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
TO 1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
TO 1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
TO 1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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Todres E.Z., Nardi J.B., Robertson H.M.;

Todres E.Z., Nardi J.B., Robertson H.M.;

The tectraspanin superfamily in insects.";

Submitted (JW-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AF274013; AAF90139.1; -..

ENBL, AF274013; AAF90139.1; -..

Interpro, IPR000301; Transmem—4.

Pfam; PP00315; transmembrane4; 1.

PRINTS; PR00259; TMFOUR.

SEQUENCE 274 AA; 31141 MW; FD03CC5D50B63018 CRC64;
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CI 212
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November 21, 2003, 13:41:43 ; Search time 20 Seconds (without alignments) 1120.365 Million cell updates/sec
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1283
1 MPGKHQHFQEPEVGCCGKYF......RAPYTPKAVWASLRSGCRTT 233
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Perfect score:
Sequence:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000 PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

283308

Total number of hits satisfying chosen parameters:

283308 segs, 96168682 residues

Searched:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	tetraspan TSPAN-5	hypothetical prote	hypothetical prote		tetraspan TSPAN-6	T-cell acute lymph	tetraspan TSPAN-6	hemopoietic cell s	-	tumor-associated a	metastasis suppres			880	CD63 antigen - rah	CD63/ME491 antigen	cell surface prote	antigen - mouse	cell surface prote	CD9 antigen - rat	Ω	٠	ے	surface	_	antigen -	integral m		tetraspan TSPAN-2
SUMMARIES		OI OI	A59261	T24912	T32652	A59265	A59258	139368	A59260	A37243	A39574	A36056	A46493	843511	149561	138016	JC2297	A46508	A46472	149589	A35649	S39262	T21696	A42929	A40402	B47629	A43522	JX0221	A40181	92	A59263
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hypothetical protein T14G10.6 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Dacession: T24912 R;Wild, A. submitted to the EMBL Data Library, January 1996 A;Reference number: Z19954 A;Accession: T24912 A;Accession: T24912 A;Accession: Preliminary; translated from GB/EMBL/DDBJ

	11.7.5	241 242 233 223			tetraspan TSPAN-1 hypothetical prote hypothetical prote hypothetical prote sarcoma amplified
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			,	ALIGNMENTS	
SULT 1 9261 traapan TSPAN-5 Species: Home sa Date: 19-May-200 Accession: A5926 Told, S.C.; Doct Tille: Sequences Reference number Accession: A5926 Status: prelimin Molecule type: D Residues: 1-264 Genetics: Genetics: Genetics:	RESULT 1 A59261 tetraspan TSPAN-5 - human C; Species: Homo sapiens (man) C; Accession: A59261 R; Todd, S.C.; Doctor, V.S.; Levy, S. Biochim. Biophys. Acta 1399, 101-104, 1 A; Title: Sequences and expression of si, A, Accession: A59261 A, Accession: A59261 A, Status: preliminary; not compared with A, Molecule type: DNA A, Residues: 1.264 aTOD> A, Residues: 1.264 aTOD> A, Gross-references: GB:AF053455; NID:G2' C; Genetics: A, Gene: TSPAN-5 C; Superfamily: CD9 antigen	n (man) Luence_ 399, 1 Xyress 58; Mu ot com	red 101 11D 11D 17D 15;	19-May-2000 #text_cha 998 x new members of the 78; PMID:9714763 h conceptual translat h conceptual translat	nge 02-Jun-2000 tetraspanin/TM4SF family ion .1; PID:g2995865
Query Match Best Local Simi Matches 151;	/ Match Local Similarity hes 151; Conserva	66.4%; 77.8%; ative		Score 852; DB 2; Length Pred. No. 6.5e-66; 6; Mismatches 21; Indel	264; 8 6; Gaps 2;
1 MPG 1 MSG	KHOHFOE :: KHYKG	PBVGCC PEVSCC	8-5	MPGKHQHPQEPEVGCCGKYFLFGFNIVFWVLGALFLAIGLWAMGEKGVLSNISALTDLGG -	GVLSNISALTDLGG 60 GVLSNISSITDLGG 58
61 LDP	VWLFVVV VWLFLVV	GGVMSV : GGVMFI	2=2	LDPVWLFVVVGGVMSVLGFAGCIGALRENTFLLKFPSVFLGLIFFLELATGILAFVF 	SVFLGLIFFLELATGILAFVFKDW 120
121 IRD : 115 IKD	OLNFFIN 	NNVKAY :: NNIRAY	2 — Z	IRDQLNFFINNNVKAYRDJIDLQNLIDFAQEYWSCCGARGPNDWNLNIYFNCTDLNPSRE -	NIYFNCTDLNPSRE 180 NIYFNCTDSNASRE 174
81 RCG 	CGVPFSCCVRDPA		194		

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A,Gene: TSPAN-6
C;Superfamily: CD9 antigen
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenore, J.
Sansone, Z21206
A;Cession: T33652
A;Reference number: Z21206
A;Reference number: Z21206
A;Reference number: Z21206
A;Redesion: T33652
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Redesion: T33652
A;Redesion: T33652
A;Redesion: T33652
A;Redesion: Sansone, J.
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A;Gene: CESP:F39C12.3
A;Map posttion: X
A;Introns: 42/3; 104/3; 133/3; 164/3; 213/3; 276/3; 336/3
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                                                                                                                                                                                                                                                                                                                                                                                                                68 VVVGGVMSVLGFAGCIGALRENTFLLKFFSVFLGLIFFLELATGILAFV--FKDWIRD-Q 124
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                                                                                                                                                                                                                                                         12 EVGCCGKYFLFGFNIVFWVLGALFLAIGLWA----WGEKGVLSNISALTDLGGLDPVWLF
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Best Local Similarity 33.6%; Pred. No. 8.1e-17;
Matches 72; Conservative 40; Mismatches 78; Indels
                                                                                                                                                                                              Indels
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A;Residues: 1-308 <WIL>
A;Cross-references: EMBL:Z68880
A;Experimental source: clone T1
C;Genetics:
A;Gene: CESP:T14G10.6
A;Map position: 4
A;Introns: 20/3; 53/1; 283/3
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CI 212
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RESULT 4 A59265

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tetraspan TSPAN-4 - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: A52265
R;Todd, S.C.; Doctor, V.S.; Levy, S.
Biochin. Biophys. Acta 1399, 101-104, 1998
A;Title: Sequences and expression of six new members of the tetraspanin/TM4SF family. A;Reference number: A59258; MUID:98390278; PMID:9714763
A;Reference number: A59258; MUID:98390278; PMID:9714763
A;Residues: TSPAN-4
A;Residues: 1-238 <TOD>
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A;Residues: 1-238 <TOD>
A;Genetics: GB:AF054841; NID:g2997746; PIDN:AAC69717.1; PID:g2997747
C;Superfamily: CD9 antigen
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R,Todd, S.C.; Doctor, V.S.; Levy, S.
Biochim. Biophys. Acta 1399, 101-104, 1998
A;Title: Sequences and expression of six new members of the tetraspanin/TM4SF family. A,Reference number: A59258; MUID:98390278; PMID:9714763
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78 GFAGCIGALRENTFILLKFFSVFLGLIFFLELATGILAFVFKDWIRDQLNFFINNNVKAY- 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              137 -RDDIDLONLIDFAQEYWSCCGARGPNDWNLNIYFNCTDLNPSRERCGVPFSCCVRDPAM 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 TOGNVGLTNAWSIIQTDFRCCGVSNYTDW-FBVY-----NATR----VPDSCC----L 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 IRDQLNFFINNNVKA---YRDDIDLQ-NLIDFAQEYWSCCGARGPNDWNLNIYFNCTDLN 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C.S.ecies: Homo sapiens (man)
C.Late: 19-May-2000 #sequence_revision 19-May-2000 #text_change 02-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 KYLMFAFNLLFWLGGCGVLGVGIWLAATQGSFATLS--SSFPSLSAANLLITGAFVMAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 KYFLFGFNIVFWVLGALFLAIGLWAWGEKGVLSNISALTDLGGLDPVWLFVVVGGVMSVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MPGKHQHFQEPEVGCCGKYFLFGFNIVFWVLGALFLAIGLWAWGEKGVLSNISALTDLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 18.9%; Score 243; DB 2; Length 238;
1 Similarity 29.7%; Pred. No. 1.2e-13;
62; Conservative 33; Mismatches 90; Indels 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18.7%; Score 240.5; DB 2; Length 245; 31.6%; Pred. No. 2.1e-13; 10. 10. Mismatches 83; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; not compared with conceptual translation A;Molecule type: mRNA
A;Residues: 1-245 <TOD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 196 SSTPSVAMMSGSNWSWSSRAP-YTPKAVW 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EFSESCGLHAPGTW-W--KAPCYETVKVW 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 31.6%;
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A;Reference number: A59258; MUID:98390278; PMID:9714763
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                                                                                                                                                                                                                                                                                                                                                                                                      56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180 ERCGVPFSCC 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---GFPKSCC 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C, Accession: A37243; A45872
                                                                                                                                                                                                                                 A;Gene: Tspan~6
C;Superfamily: CD9 antigen
                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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A;Molecule type: mRNA
A;Residues: 1-219 <ANG>
                                         A; Accession: A59260
                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                   Best Local
Matches 5
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                                                                                                                                                                           Tabous (Caberate names: cell surface glycoprotein (clone A15); TALLA-1 (Caberate names: cell surface glycoprotein (clone A15); TALLA-1 (Caberate names: cell surface glycoprotein (clone A15); TALLA-1 (Caberate names: cell surface glycoprotein (clone A15); TALLA-1 (Caberate names: Homo spatiens (man) (Caberate names: Homo spatiens (man) (Caberate names: Homo spatiens (man) (Caberate names: Homo spatiens (man) (Caberate names: 13976# Hagquance_revision 23-Aug-1996 #text_change 22-Jun-1999 (Caberate names: 13976# 15476# (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) (Man) 
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tetraspan TSPAN-6 - mouse

(Species: Mar musculus (house mouse)

C) Accession: A59260

E) Accession: A59260

E) Accession: A59260

E) Accession: A59260

E) Accession: A59260

E) Accession: A59260

E) Accession: A59260

E) Accession: A59260

E) Accession: A59260

E) Accession: Accession of six new members of the tetraspanin/TM4SF family.
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F/103-207/Domain: extracellular #status predicted <EX2>
F/103-207/Domain: extracellular #status predicted <EX2>
F/208-232/Domain: transmembrane #status predicted <TM4>
F/233-24/Domain: incracellular #status predicted <TM3>
F/49/150,153,172,183/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGKYFLFGFNIVFWVLGALFLAIGLWAWGEKGVLSNISALTDLGGLDPVWLFVVVGGVMS 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YRDDIDLQNLIDFAQEYWSCCGARGPNDWNLNIYFNCTDLNPSRERCGVPFSCCVRD 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12;
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177 PSRERCGVPFSCC 189
                                                          167 YYSEK-GFPKSCC 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16
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v; Title: Identification and analysis of cDNA clones encoding CD53. A pan-leukocyte antiv; Reference number: A37243; MUID:91079522; PMID:2258620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A/Molecule type: mRNA
A/Residues: 1-219 <AMI>
A/Cross-references: GBM160871; NID:g180140; PIDN:AAA51951.1; PID:g180141
A/ACTOSS-references: GBM60871; NID:g180140; PIDN:AAA51951.1; PID:g180141
A/Angelisova, P.; Vlcek, C.; Stefanova, I.; Lipoldova, M.; Horejsi, V.
Immunogenetics 32, 281-285, 1990
A/Title: The human leucocyte surface antigen CD53 is a protein structurally similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 LDPVWLFVVVGGVMSVLGFAGCIGALRENTFLLKFFSVFLGLIFFLELATGILAFVFKDW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 IRDQLNFFINNNVKAYRDDIDLQN-LIDFAQEYWSCCGARGPNDWNLNIYFNCTDLNPSR 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MPGKHQHFQEPEVGCCGKYFLFGFNIVFWVLGALFLAIGLWAWGEKGVLSNISALTDLGG 60
A;Status: preliminary; not compared with conceptual translation A;Molecule type: mRNA A;Molecule type: mRNA A;Residues: 1-245 <TOD>
A;Cross-references: GB:AF053454; NID:g2995862; PIDN:AAC69711.1; PID:g2995863 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hemopoietic cell surface glycoprotein CD53 - human
N;Alternate names: pan-leukocyte surface antigen CD53
C;Species: Homo sapiens (man)
C;pacies: 30-Dec-1991 #sequence_revision 09-Aug-1996 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: GB: M37033; NID: 9180142; PIDN: AAA35663.1; PID: 9180143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;129,148/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                             13;
                                                                                                                                                                                                                                                                                                                                                     18.7%; Score 239.5; DB 2; Length 245; 29.5%; Pred. No. 2.5e-13; Live 32; Mismatches 89; Indels 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18.4%; Score 235.5; DB 1; Length 219; 31.0%; Pred. No. 5e-13;
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F;1-10/Domain: intracellular #status predicted <CY1-
F;1-54/Domain: transmembrane #status predicted <TM1-
F;37-54/Domain: extracellular #status predicted <TM2-
F;55-75/Domain: transmembrane #status predicted <TM2-
F;76-80/Domain: intracellular #status predicted <CY2-
F;81-106/Domain: transmembrane #status predicted <TM3-
F;107-181/Domain: extracellular #status predicted <TM3-
F;107-181/Domain: intracellular #status predicted <TM3-
F;05-219/Domain: intracellular #status predicted <TM3-
F;05-219/Domain: intracellular #status predicted <TM3-
F;05-219/Domain: intracellular #status predicted <CY3-
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A/Gross-references: GDB:127521; CMIM:151525
A/App position: 1p21-1p13.3
C/Superfamily: CD9 antigen
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A;Status: nucleic acid sequence not shown; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-26.
A;Cross-references: EMBL:U20770; NID:g806805; PIDN:AAC50133.1; PID:g806806
R;Gaugitech, H.W.; Hofer, E.; Huber, N.E.; Schnabl, E.; Baumruker, T.
Br. J. Immunol. 21, 377-383, 1991
A;Title: A new superfamily of lymphoid and melanoma cell proteins with extensive homolo-A;Reference number: S16156; MUID:91153380; PMID:1842498
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A;Note: the authors translated the codon AGC for residue 50 as Thr
B;Imai, T.; Fukudome, K.; Takagi, S.; Nagira, M.; Furuse, M.; Fukuhara, N.; Nishimura, I
J. Immunol. 149, 2879-2866, 1992
A;Title: C33 antigen recognized by monoclonal antibodies inhibitory to human T cell leul
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C;Date: 18-Jun-1993 #sequence_revision 09-Aug-1996 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: 138942; SI6156; A46493
R;Dong, J.T.; Lamb, P.W.; Rinker-Schaeffer, C.W.; Vukanovic, J.; Ichikawa, T.; Isaacs, Scance 268, 884-886, 1995
A;Title: KAII, a metastasis suppressor gene for prostate cancer on human chromosome 11p A;Reference number: 138942; MUID:95273964; PMID:7754374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 VWLFVVVGGVMSVLGFAGCIGALRENTFLLKFFSVFLGLIFFLELATGILAFVFKDWIRD 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; restandes: 1-23, cs.dx.
A; Cross-references: GB:M3252; NID:g180925; PIDN:AAA35709.1; PID:g180926
C; Genetics:
A; Gene GBB:TW48F3
A; Cross-references: GDB:9113496; OMIM:600769
C; Superfamily: CD9 antigen
C; Reywords: glycoprotein; transmembrane protein
C; Reywords: glycoprotein; transmembrane predicted (CVI)
F; 12-33/Domain: intracellular #status predicted (TMI)
F; 34-52/Domain: extracellular #status predicted (TMI)
F; 34-52/Domain: extracellular #status predicted (TMI)
F; 34-52/Domain: transmembrane #status predicted (TM2)
F; 98-107/Domain: transmembrane #status predicted (TM3)
F; 108-205/Domain: transmembrane #status predicted (TM3)
F; 206-232/Domain: intracellular #status predicted (TM4)
F; 233-237/Domain: intracellular #status predicted (TM4)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 VGCCGKYFLFGFNIVFWVLGALFLAIGLWA------WGEKGVLSNISALTDLGGLDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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A;Residues: 1.-239,'NV',242-267 <IMA>
A;Cross-references: GB:S48196; NID:g258294; PIDN:AAB23825.1; PID:g258295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116 IVNETLYENTKLLSATGESEKOFÓBAÍIVFÖÉBFKCCGLVNGAADWGNN 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67; Indels
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A;Reference number: A46493; MUID:93017900; PMID:1401919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18.0%; Score 231; DB 1;
33.1%; Pred. No. 1.3e-12;
tive 24; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Status: not compared with conceptual translation
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Best Local Similarity 33.18;
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A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-267 <GAU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: A46493
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C;Species: Homo sapiens (man)
C;Date: 16-Nov-1990 #sequence_revision 09-Aug-1996 #text_change 20-Apr-2000
C;Accession: A36056
R;Szala, S.; Kasai, Y.; Steplewski, Z.; Rodeck, U.; Koprowski, H.; Linnenbach, A.J.
Proc. Natl. Acad. Sci. US.A. 87, 6833-6837, 1990
A;Title: Molecular cloning of cDNA for the human tumor-associated antigen CO-029 and ide
A;Reference number: A36056; MUID:90370878; PMID:2395876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a new family of cell surface
    5
                                                                                                                                                                                                                                                                             |: | ||:|:|| ||: | 64 MVVAFLGCMGSIKENKCLLMSFFILLLILLAEVTLAILLFVYEQKINEYVAKGLTDSIH 123
                                                                                                                                                                                                                               75 SVLGFAGCIGALRENTFLLKFFSVFLGLIFFLELATGILAFVFKDWIRDQLNFFINNNVK 134
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                                                                                                                            10 KYVLFFFNLLFWICGCCILGFGIYLLIHNNFGVLFHNLPSLT-LGN-----VFVIVGSII 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Leukovice aiu.1991 #Sequence_revision 09-Aug-1996 #text_change 22-Jun-1999 C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Accession: A39574
R;Bellacosa, A; Lazo, P.A.; Bear, S.E.; Tsichlis, P.N.
Mol. Cell. Biol. 11, 2864-2872, 1991
A;Title: The rat leukocyte antigen MRC OX-44 is a member of a new family of C/A;Reference number: A39574; MUID:91203909; PMID:2017181
A;Reference number: A39574; MUID:91203909; PMID:2017181
A;Reference number: A39574; MUID:91203909; PMID:2017181
A;Reference number: A39574; MUID:91203909; PMID:2017181
C;Superfamily: CD9 antigen
C;Superfamily: CD9 antigen
C;Superfamily: CD9 antigen
C;Reywords: glycoprotein; transmembrane protein
C;Reywords: glycoprotein; transmembrane predicted <CX1>
F;11-36/Domain: intracellular #status predicted <CX1>
F;57-73/Domain: extracellular #status predicted <CX2>
F;80-106/Domain: intracellular #status predicted <CX2>
F;80-106/Domain: transmembrane #status predicted <CX3>
F;107-181/Domain: extracellular #status predicted <CX3>
F;107-181/Domain: transmembrane #status predicted <CX3>
F;107-181/Domain: transmembrane #status predicted <CX3>
F;107-181/Domain: transmembrane #status predicted <CX3>
F;107-181/Domain: intracellular #status predicted <CX3>
F;205-219/Domain: intracellular #status predicted <CX3>
F;107-181/Domain: intracellular #status predicted <CX3>
F;107-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 KYVLFFFNFLFWVCGCCILGFGIHLLVQNTYGILFRNLPFLT-IGN-----VLVIVGSII 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Species: Ratius norvegicus (Norway rat)
Date: 30-Aug-1991 #sequence_revision 09-Aug-1996 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;119,129,148/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                              KYFLFGFNIVFWVLGALFLAIGLW - - AMGEKGVL - SNISALTDLGGLDPVWLFVVVGGVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1, Length 219;
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1 Similarity 32.8%; Pred. No. 7.4e-13;
63; Conservative 24; Mismatches 70; Indels
64; Indels
31; Mismatches
54; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---- PSGADVQG 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          leukocyte antigen OX-44 - rat
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Men Nov

A;Gene: GDB:KAI1

Query Match

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C;Accession: 149561
R;Nagira, M.; Imai, T.; Ishikawa, I.; Uwabe, K.I.; Yoshie, O.
R;Nagira, M.; Imai, T.; Ishikawa, I.; Uwabe, K.I.; Yoshie, O.
A;Title: Mouse homologue of C33 antigen (CD82), a member of the transmembrane 4 superf A;Reference number: 149561; MUID:94313678; PMID:8039242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  melanoma-associated antigen CD63 [validated] - human
NAlternate names: antigen ME491; lysosomal membrane glycoprotein CD63; ME491/CD63 ant
C;Species Homo sapiens (man)
C;Decies Homo sapiens (man)
C;Decies Homo sapiens (man)
C;Date: 17-May-1996 #sequence revision 09-Aug-1996 #text change 08-Dec-2000
C;Accession: 138016; S01418; A39514; B35826; A61177; A61173; A56782
R;Hotta, H.; Miyamoto, H.; Hara, I.; Takahashi, N.; Homma, M.
Biochem. Biophys. Res. Commun. 185, 436-442, 1992
A;Title: Genomic structure of the ME491/CD63 antigen gene and functional analysis of t
A;Reference number: 138016; MUID:92287132; PMID:1599482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-238 <RES.
A; Residues: 1-238 <RES.
A; Cross-references: EMB: X62654; NID: 9430755; PIDN: CAA44519.1; PID: 9430756
R; Hotta, H.; Ross, A.H.; Huebner, K.; Isobe, M.; Wendeborn, S.; Chao, M.V.; Ricciardi, Cancer Res. 48, 2955-2962, 1988
A; Title: Molecular cloning and characterization of an antigen associated with early st
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A;Molecule type: mRNA
A;Residues: 1-238 <+MOT>
A;Residues: 1-238 <+MOT>
A;Residues: 1-238 <+MOT>
A;Residues: 1-238 <+MOT>
A;Residues: 1-238 <+MOT>
A;Cross_references: EMBL:X07982; NID:g34526; PIDN:CAA30792.1; PID:g34527
B;Metzelaar, M.J.; Wijngaard, P.L.J.; Peters, P.J.; Sixma, J.J.; Nieuwenhuis, H.K.; Cl J. Biol. Chem. 266, 3239-3245, 1991
J. Biol. Chem. 266, 3239-3245, 1991
A;Title: CD63 antigen. A novel lysosomal membrane glycoprotein, cloned by a screening A;Reference number: A39514; MUID:91131632; PMID:1993697
                                                                                                                                                 65 FLVAFVGCCGACKENYCLMITFAIFLSLIMLVEVAVAIAGYVFRDQVKSEFNKSFQQMQ 124
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                                                                                               75 SVLGFAGCIGALRENTFLLKFFSVFLGLIFFLELATGILAFVFKDWIRDQLNFFINNNVK 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                    135 AYRDDIDLQNLIDFAQEYWSCCGARGPNDWNLNIYFNCTDLNPSRERCGVPFSCCV 190
                                                                                                                                                                                                                                                                                                                          125 NYLKDNKTATILDKLQKENNCCGASNYTDWE-NI------PGMAKDRVPDSCCI 171
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C; Superfamily: CD9 antigen
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A;Molecule type: mRNA
A;Residues: 1-266 <RES>
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Best Local Similarity
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R;Miyamoto, H.; Homma, M.; Hotta, H.
Biochim. Blophys. Acta 1217, 312-316, 1994

A.Title: Molecular cloning of the murine homologue of CD63/ME491 and detection of its st A;Reference number: S43511, MUID:94198294; PMID:8148377

A;Recession: S45511

A;Reference number: S43511; MUID:94198294; PMID:8148377

A;Recission: S45511

A;Residues: 1-238 «MIY»

A;Residues: 1-238 «MIY»

A;Residues: 1-238 «MIY»

A;Residues: 1-238 mily: D16432; NID:9484052; PIDN:BAA03904.1; PID:9976238

C;Superfamily: CD9 antigen

C;Superfamily: CD9 antigen

C;Superfamily: CD9 antigen

C;Superfamily: extracellular #status predicted «CXI»

F;12-35/Domain: transmembrane #status predicted «EXI»

F;36-51/Domain: transmembrane #status predicted «EXI»

F;36-51/Domain: transmembrane #status predicted crivial predicted crivial predicted crivial contains intracellular #status predicted crivial crivial crivial minimization predicted crivial crivial crivial minimization minimization predicted crivial crivial minimization minimization predicted crivial crivial minimization minimization predicted crivial crivial minimization minimization predicted crivial crivial minimization minimization predicted crivial crivial minimization minimization minimization minimization minimization minimization minimization minimization minimization minimization minimization minimization minimization minimization minimization minimization minimization minimization minimization minimization minimization minimization minimization minimization minimization minimization minimization minimization minimization minimization minimization minimization minimization minimization minimization minimization minimization minimization minimization minimization minimization minimization minimization minimization minimization minimization minimization minimization minimization minimization minimization minimization minimization minimization minimization minimization minimization minimization minimization minimimization minimization minimization minimization minimization mini
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134 KAY---RDDIDLQNLIDFAQEYWSCCGARGPNDWNLNIYFNCTD----LNPSRERCGVPF 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RDYNSSRED-SLODAWDYVQAQVKCCG-----W--VSFYNWTDNAELMN--RPEVTYPC 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 CGKYFLFGFNIVFWVLGALFLAIGLWAWGEKGVLSN-ISALTDLGGLDPVWLFVVVGGVM 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;109-227/Domain: extracellular #status predicted <EX2>
F;228-252/Domain: transmembrane #status predicted <TM4>
F;253-265/Domain: intracellular #status predicted <CY3>
F;129,157,198/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CD63/ME491 antigen homolog - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 09-Aug-1996 #text_change 16-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 KYFLFGFNIVFWVLGALFLAIGLWAWGEK----GVLSNISALTDLGGLDPVWLFVVVGGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             = :: : = - ::
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCCVR---DPAMSSTPSVAMMSGSNWSWSSRAPYTPKAVWASLRSGC 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17.8%; Score 228; DB 1; Length 267; 30.0%; Pred. No. 2.7e-12; Ative 37; Mismatches 88; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
17.1%; Score 220; DB 1; Length 238;
Best Local Similarity 31.2%; Pred. No. 1.2e-11;
Matches 55; Conservative 31; Mismatches 76; Indels
Experimental source: T-cell line MOLT-4 (NCBIP:117149)
                                                                                                                                                           A.Cross-references: GDB:134216; OMIM:600623
A;Map position: 11p11.2-11p11.2
C;Superfamily: CDB antigen
C;Superfamily: CDB antigen
C;Keywords: glycoprotein; transmembrane protein
F;1-10/Domain: intracellular #status predicted <CYI>F;11-36/Domain: extracellular #status predicted <TMI>F;38-77/Domain: extracellular #status predicted <TMI>F;88-78/Domain: intracellular #status predicted <TMI>F;88-78/Domain: intracellular #status predicted <CYI>F;84-108/Domain: transmembrane #status predicted <CYI>F;84-108/Domain: transmembrane #status predicted <CYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 30,0%
Matches 68; Conservative
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completed: November 21, 2003, 13:45:26
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A; Cross-references: GB:M59907; NID:g189383; PIDN:AAA63235.1; PID:g189384
A; Cross-references: GB:M59907; NID:g189383; PIDN:AAA63235.1; PID:g189384
A; Note: the authors did not translate the codons for residues 205 through 224
B; Azorsa, D.O.; Hyman, J.A.; Hildreth, J.E.K.
Blood 78, 280-284, 1991
A; Title: CG5/PItgp40: a platelet activation antigen identical to the stage-specific, A; Accession: A61177; MUID:91300080; PMID:2070066
A; Accession: A61177
                                                                                                          R;Rapp, G.; Freudenstein, J.; Klaudiny, J.; Mucha, J.; Wempe, F.; Zimmer, M.; Scheit, DNA Cell Biol. 9, 479-485, 1990
A;Title: Characterization of three abundant mRNAs from human ovarian granulosa cells. A;Reference number: A35826; MUID:91025550; PMID:2171551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74 MSVLGFAGCIGALRENTFLLKFFSVFLGLIFFLELATGILAFVFKDWIRDQLNFFINNNV 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134 KAYRDDIDLONLIDFAQEYWSCCGARGPNDWNLNIYFNCTDLNPSRERCGVPFSCCVRDP 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENYPRONHTASILDRAGADFKCCGAANYTDW------EKIPSMSKNRVPDSCCI--- 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGKYFLFGFNIVFWVLGALFLAIGLWAWGEKGVLSN--ISALTDLGGLDPVWLFVVVGGV 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CVKFLLYVLLLAFCACAVGLIAVGV---GAQLVLSQTIIQGATP-GSLLPV-VIIAVGVF 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: GDB:CD63; MLA1
A;Caos-references: GDB:120186; OMIM:155740
A;Map position: 12q12-12q13
A;Introns: 22/3; 85/3; 110/3; 142/3; 189/3; 217/3
C;Superfamily: CD9 antigen
C;Keywords: glycoprotein: ly60some; surface antigen; transmembrane protein
F;2-238/Product: melanoma-associated antigen ME491 #status experimental <MAT>
F;2-11/Domain: intracellular #status predicted <CY1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;130,150,172/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Molecule type: protein
Residues: 2-8, X', 10-16, XX', 19-21 <HIL>
Mang, M.X.; Earley Jr., J.J.; Shields, J.A.; Donoso, L.A.
Mang, M.X.; earley Jr., 1992
rch. Ophthalmol. 110, 399-404, 1992
; Title: An ocular melanoma-associated antigen. Molecular characterization.
Reference number: A56782; MUID:92181348; PMID:1339263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;Molecule type: mRNA
;Residues: 1-238 «WAN>
;Cross-references: GB:S93788; NID:g246538; PIDN:AAB21617.1; PID:g246539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Experimental source: uveal melanoma
A;Note: sequence extracted from NCBI backbone (NCBIN:93788, NCBIP:93790)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16.7%; Score 214; DB 1; Length 238; 28.1%; Pred. No. 3.8e-11; ive 37; Mismatches 83; Indels ::
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /Domain: transmembrane #status predicted <TM3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-15/Domain: transmembrane #status predicted <TMl> | 551/Domain: extracellular #status predicted <EXI> | 52-76/Domain: transmembrane #status predicted <TM2 | 77-80/Domain: intracellular #status predicted <CYP>
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Best Local Similarity 28.1%
Matches 61; Conservative
                                                                                   Cross-references: GB:M58485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Accession: A61173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: A56782
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C;Species: Oryccolagus cuniculus (domestic rabbit)
C;Date: 28-Oct-1994 #sequence_revision 09-Aug-1996 #text_change 16-Jun-2000
C;Date: 28-Oct-1994 #sequence_revision 09-Aug-1996 #text_change 16-Jun-2000
C;Date: 28-Oct-1994 #sequence_revision 09-Aug-1996 #text_change 16-Jun-2000
R;Accession: 7: Suzuki, T:; Sasano, H:; Nagura, H:; Nose, M:; Yamamoto, T.
Cell Struct. Funct. 19, 219-225, 1994
A;Title: Increased mRNA for CD63 antigen in atherosclerotic lesions of Watanable herit
A;Reference number: JC2297; MUID:95120837; PMID:7820873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;81-103/Domain: transmembrane #status predicted <TM3>
F;104-203/Domain: extracellular #status predicted <EX2>
F;030-228/Domain: transmembrane #status predicted <TM4>
F;222-238/Domain: intracellular #status predicted <TM3>
F;225-130,150,172/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 FLVAFVGCCGTCKENYCLMITFAIFLSLIMLVEVAAAIAGYVFRDKVMSEPNKDFRQQMQ 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 CGKYFLFGFNIVFWVLGALFLAIGLWAWGEKGVLS-NISALTDLGGLDPVWLFVVVGGVM 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           surface antigen; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Molecule type: mRNA
A,Residues: 1-238 <SOH>
A,Cross-references: DDBJ:D21264; NID:g684973; PIDN:BAA04804.1; PID:g684974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    135 AYRDDIDLQNLIDFAQEYWSCCGARGPNDWNLNIYFNCTDLNPSRERCGVPFSCCV 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 NYSTDNQTALILDRWQKDFTCCGAANYTDW-----ATIPGMTRDR--VPDSCCV 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16.7%; Score 214; DB 1; Length 238; 31.2%; Pred. No. 3.8e-11; tive 32; Mismatches 75; Indels
                                                                       ---FNEKAIH---KEGC 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;12-35/Domain: transmembrane #status predicted <TMl>F;85-51/Domain: extracellular #status predicted <EXI>F;52-76/Domain: transmembrane #status predicted <TM2-F;77-80/pomain: intracellular #status predicted <CY2>
194 AMSSTPSVAMMSGSNWSWSSRAPYTPKAVWASLRSGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;1-11/Domain: intracellular #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Experimental source: aorta
C, Superfamily: CD9 antigen
C, Keywords: glycoprotein: lysosome;
                                                                           ---NVTVGCGIN---
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Matches 55; Conservative
                                                                           172
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November 21, 2003, 13:34:37; Search time 40 Seconds (without alignments) 924.582 Million cell updates/sec
                                                                                                                                                                                                                                                                                                            1 MPGKHQHFQEPEVGCCGKYF......RAPYTPKAVWASLRSGCRTT 233
                                                                                                                                                                                                               1107863
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                        1107863 seqs, 158726573 residues
                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                           OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
                                                                                                           US-09-972-970-4
1283
                                                                                                           Title:
Perfect score:
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                                                                                                                                 Sequence:
                                                                                                                                                                                        Searched:
                                                                Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	10	669	4	-	22	AAU39073	Human secreted pro
	#:	669	54.5	193	23	ABB55782	Human polypeptide
	77	5.05	ν o	z) c	77	ABP98695	Kat gamma-nydroxyb
	14	5.86	9	4 (22	AAB87034	Human secreted pro
	15	638.5	0	1 101	23	AAE18535	Human tetraspan pr
	16	637.5	O.	CA	22	AAB87134	Human secreted pro
	17	635.5	0 0	C) I	55	AAB87135	Human secreted pro
	2 5	634.5	ν σ	40	2 6	ABG2/829 AAB87136	Novel numan diagno Human secreted pro
	20	634.5	Š	1 (1)	22	AAB87137	Human secreted pro
	21	625.5	8	(4)	21	AAY76133	Human secreted pro
	27	619.5	300	N C	5 5	AAB23036	Human tetraspanin-
	24	514.5	~ ~	40	7 6	AAB8 7039	Novel human diagno
	25	515.5	0	1 (7)	55	AAB87035	Human mature TANGO
	26	482.5	7		21	AAY83082	F-box protein FBP-
	27	482.5	~ 1	(23	AA022468	Human F-box protei
	9 6	482.5	~ u	N C	7 0	ABB64234	Urosophila melanog
	30	471.5	o w	4 (4	23	ABP69619	Human polypeptide
	31	453.5	S	-	22	AAB87037	Human TANGO 339 tr
	32	437.5	₩.	e	23	ABB89649	Human polypeptide
	33	429	m	-	55	AAG75522	Human colon cancer
	34	425	m	(4)	57	AAB12120	Hydrophobic domain
	35	421.5	N C	N C	7 5	ABB60781	Drosophila melanog
	0 6	412.5	v c	40	7 6	AAEU00/1	Human gene 31 enco
	38	412.5	N	101	2 2	AAY87094	Human secreted pro
	39	411.5	N	· CN	21	AAB23047	Human tetraspanin-
	40	411.5	N	m	22	ABB65216	Drosophila melanog
	41	383	0	~	22	AAB49510	Clone HE8EL16 #2.
	27	373	σ,	α,	22	ABG16481	Novel human diagno
	43	331	S I	- 1 с	21	AAY64846	Human 5' EST relat
	. 4	324	n u	40	, 5	AAW 10313 AAW 99374	procein 1311 (IN
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						ALIGNMENTS	
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A. 1.	.13218		•				
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AC	AAE1	13218;					
ž i	- 4	:	•				
ž	12-F	-FEB-2002	=======================================	(first entry)	2		
	Human	in gene	1 enc	encoded TM4SF	SF r	receptor protein HOFOB55	155, SEQ ID NO:4.
	Huma	in; 4-tr	ansme	mbrane s	uper	family; TM4SF recepto	r; breast cancer;
	OVAL	lan can	cer;	ımmune o	1801	der; Addison's diseas	nealing;
	diab	e tilerap	y, au llitu	icolmmune 18: aller	7 11 de	molytic anaemia; auto Grobn's disease: mult	na; aucolmmune inyroiditis; Be: multiple sclerosis:
	rhen	matoid	arthr	itis; ul	cera	tive colitis; cardiov	disorder
	myoc	ardial	scha	emia; ne	urol	odical disease; antif	ntivir
	anti	bacteri	al; c	erebral	anox	antibacterial; cerebral anoxia; epilepsy; infecti	ase;
	3116	י המדמח.		ancer.			
SO	Ношо	sapiens					
Y E	Key			Location	/Qua	lifiers	
T.	Regi	no.		158164			
<u>.</u> .	, Lugar	5		/note= "	Immr	nogenic epitope"	
: E	F.	į		/note= "	Immu	nogenic epitope"	
H	Region	no		212218			
F 5	,	;		/note= "	Immu	nogenic epitope"	
FT	ved ton	10		/note= "Immunogenic	Immu	mmunogenic epitope"	
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PN	W020	WO200177173-A1	-A1.				

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Human; 4 transmembrane superfamily receptor protein;
endocrine; cardiovascular; cerebrovascular disease; neural disorder;
reproductive; skin; renal system; autoimmune; hyperproliferative; ocular;
bacterial infection; viral; fungal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           encoding human soluble 4 transmembrane superfamily receptor protein (see AAC90012-C90023 and AAB49502-B49513). The present sequence is one such protein. The present protein can be used to screen for binding partners and molecules which modify its activity. Antibodies specific for the present protein can be used to treat and/or prevent diseases associated with abberant expression or activity of the present protein e.g. endocrine disorders e.g. Addison's disease, (cardio) vascular diseases e.g. arrhythmia and atherosclerosis, cerebrovascular diseases incural disorders e.g. Alzheimer's and Parkinson's disease, reproductive disorders e.g. psoriasis, renal system disorders e.g. neural nephritis, (auto) immune system disorders e.g. graft vs. host disease, hyperproliferative disorders e.g. neoplasms of the pancreas, ocular disorders e.g. graft vs. host disease, hyperproliferative disorders e.g. neoplasms of the pancreas, viruses and disorders e.g. graft vs. viruses and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated nucleic acid molecule encoding human soluble 4 transmembrane superfamily receptor protein, useful for diagnosing, treating and/or preventing disorders e.g. Alzheimer's, cancer and arrhythmia -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MPGKHQHFQEPEVGCCGKYFLFGFNIVFWVLGALFLAIGLWAWGEKGVLSNISALTDLGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present invention relates to isolated nucleic acids and proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roschke V, Shi Y, Komatsoulis GA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1066; DB 22;
Pred. No. 1.2e-104;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 11; Pages 280-281; 297pp; English.
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03-JUN-1999; 99US-0137797.
11-JUN-1999; 99US-013873.
18-MUS-1999; 99US-0149447.
28-JAN-2000; 2000US-0178770.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                            18-MAY-2000; 2000WO-US13504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fan P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 99.5
Matches 193; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ni J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAC90014
                                                                                                                                                                             WO200070076-A1
                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ruben SM,
Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptor polypeptides and polynuclecides. Sequence of the invention receptor polypeptides and polynuclecides. Sequence of the invention are useful for preventing, treating, ameliorating or diagnosing a pathological condition. TMASP polypeptides are useful for screening molecules which modify their activity. TMASP nucleic acids, protein, antibodies, agonists and antagonists are useful in the diagnosis, treatment and prevention of cancer, particularly breast and ovarian cancer, and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; immune disorders such as Addison's disease, allower, autoimmune hammolytic anaemia, autoimmune thyroiditis, allowers, and ulcerative colitis; cardiovascular disorders such as myocardial ischaemias; wound healing; neurological diseases such as myocardial ischaemias; wound healing; neurological diseases such as myocardial ischaemias; wound healing; neurological diseases such as myocardial ingene parasitic infections diseases such as viral, bacterial, fungal and parasitic infections. TMASP polynucleotides are also useful in gene therapy. The present sequence is human TMASP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                 Novel isolated protein, a member of 4-transmembrane superfamily of receptor polypeptides, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention relates to human 4-transmembrane superfamily (TM4SF)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 23; Length 233;
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100.0%; Pred. No. 9.4e-128;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11; Page 267-268; 271pp; English.
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                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC
                                                                            05-APR-2001; 2001WO-US11130.
                                                                                                                             10-APR-2000; 2000US-195336P.
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Best Local Similarity 100.
Matches 233; Conservative
                                                                                                                                                                                                                                                                       2002-017447/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            233 AA;
                                                                                                                                                                                                                            Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor protein
                                                                                                                                                                                                                                                                                                 N-PSDB; AAD21883
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                                 18-OCT-2001
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                                                                                                                                                                                                                         Shi Y,
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                                                           Tetraspanin; 23228; cell surface protein; transmembrane domain; extracellular growth factor; HB-EGF; TGF-alpha; amphiregulin; diabetes mellitus; arthritis; multiple sclerosis; encephalomyelitis; dermatitis; Crohn's disease; and asthma; cancer; metastasis; orial infection; cellular signalling activity; cell proliferation; cell motility; CD81; B-Cell antigen receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New tetraspanin 23228 polypeptide useful in screening assays, predictive medicine and as a prophylactic or therapeutic agent, e.g.,
                                                                                                                                                                                     "Extracellular loop'
                                                                                                                                                 18..263
/label= Tetraspanin_domain
                                                                                                                                                                                                                                                                    37..94
/note= "Intracellular loop'
                                                                                                                                                                                                                                                                                                     "Extracellular loop'
                                                                                                                                    ...18
'label= N-terminal_domain
                                                                                                                                                                                                                                                                                                                                                                                         /label= C-terminal_domain
                                                                                                                                                                                                   note= "N-myristoylated"
                                                                                                                                                                                                                                                            "N-myristoylated"
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                                                                                                                                                                                                           51..54
/note= "N-glycosylated"
                                                                                                                                                                                                                                                                                                                    "N-glycosylated"
                                                                                                                            Location/Qualifiers
      AAB47950 standard; Protein; 270 AA.
                                                                                                                                                                                                                        64..86
/label= TM2
71..76
                                                                                                                                                                19..43
/label= TM1
                                                                                                                                                                                                                                                                               95..117
/label= TM3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MILL-) MILLENNIUM PHARM INC
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                                                                                                                                                                                                                                                                                                                                                'label= TM4
                                                                                                                                                                                                                                                                                                                                                                                                                                    21-AUG-2001; 2001WO-US41811
                                  (first entry)
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235..256
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/note=
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                                                                                                              Homo sapiens
                                  18-JUN-2002
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                    AAB47950;
                                                                                                                                    Domain
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AAB47950
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This sequence shows tetraspanin 23228. This protein is a cell surface protein having four transmembrane domains (TM1-TM4). TM1, TM3 and TM4 that a single polar amino acid located within them, which may interact with each other and contribute to domain stability. The cytoplasmic New the ach other and contribute to domain stability. The cytoplasmic New the last ham 30 amino acids in length. The second extracellular domain action are less than 30 amino acids in length. The second extracellular domain action obstween TM3 and TM4 contains conserved Cys residues and may function to bind extracellular growth factors, such as HB-EGF, TGF-alpha and amphiregulin. The 23228 protein is useful for diagnosing and treating concephalomyelitis, dermatitis, crohn's disease and asthma; cell such as diabetes mellitus, arthritis, multiple sclerosis, encephalomyelitis, dermatitis, Crohn's disease and asthma; cell metastasis, and/or viral infections. 23228 polypeptide can control cellular signalling activity, bind to an extracellular growth factor, for example, amphiregulin, regulate cell proliferation, bind to a cell correct control activity, bind to another tetraspanin such as GD81, to associate with a metility, bind to another tetraspanin such as GD81, to association with a cell antigen receptor and the ability to modulate the association
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disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
hematopoietic and immune diseases such as diabetes or multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; transmembrane protein; cell proliferation disorder; myelom; reproductive disorder; smooth muscle disorder; neurological disord; arteriosclerosis; leukaemia; acquired immunodeficiency syndrome; Alalergy; ovulatory defect; angina; hypertension; stroke; epilepsy; Alzheimer's disease; Tourette's disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83.1%; Score 1066; DB 23; Length 270; 99.5%; Pred. No. 1.2e-104; ive 0; Mismatches 1; Indels 0;
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                                                                                                     Claim 1; Page 113-14; 123pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 193, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= '
269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    270 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Key
Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-FEB-2001
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                                sclerosis
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The invention relates to novel genes (ABL89449-ABL90853) and proteins (ABB89040-ABB90444) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are established from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune through architis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and parasitic infectious diseases such as viral, bacterial, fungal
                                        Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; anticonvulsant; antidecterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 LDPVWLFVVVGGVMSVLGFAGCIGALRENTFLLKFFSVFLGLIFFLELATGILAFVFKDW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MPGKHQHFQEPEVGCCGKYFLFGFNIVFWVLGALFLAIGLWAWGEKGVLSNIXALTDLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 IRDOLNFFINNNVKAYRDDIDLQNLIDFAQEYWSCCGARGPNDWNLNIYFNCTDLNPSRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 IRDQLNLFINNNVKAYRDDIDLQNLIDFAQEYWSCCGARGPNDWNLNIYFNCTDLNPSRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MPGKHOHPOEPEVGCCGKYFLFGFNIVFWVLGALFLAIGLWAWGEKGVLSNISALTDLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prevention of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; SEQ ID NO 2805; 2081pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel 1405 isolated polypeptides, useful for diagnosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1055; DB 23;
Pred. No. 2.3e-103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
    Human polypeptide SEQ ID NO 2805.
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98.5%;
                                                                                                                                                                                                                                                                                        18-MAY-2001; 2001WO-US16450.
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Matches 191, Conservative
                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                               Birse CE, Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-122018/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      329 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ABL90838.
                                                                                                                                                                                                       WO200190304-A2
                                                                                                                                                                                                                                                  29-NOV-2001
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                                                                                                                                                                     Ношо
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a human transmembrane proteins (HTMP). Agonists and antsgonists of the protein are used to treat a disease or condition associated with overexpression of the protein. Diseases and conditions which can be treated include cell proliferative, immunological, reproductive, smooth muscle and neurological disorders e.g. arteriosclerosis, myeloma, leukaemia, acquired immunodeficiency syndrome (AIDS), allergies, ovulatory defects, angina, hypertension, stroke, Alzheimer's disease, epilepsy and Tourette's disorder. The polynucleotides may be used to detect and quantify gene expression in biopsied tissues where protein expression may be correlated with disease e.g. to determine absence, presence or excess expression of HTMP or to monitor regulation of HTMP expression during therapeutic intervention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120
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                                                                                                                                                                                                                                                                                                                                                  Baughn MR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IRDOLNFFINNNVKAYRDDIDLONLIDFAQEYWSCCGARGPNDWNLNIYFNCTDLNPSRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                New human transmembrane proteins are used to treat a disease or condition associated with decreased expression of functional HTMP Tourette's disorder, angina and leukaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                Bandman O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                        'note= "potential phosphorylation site"
                                                                            /note= "potential phosphorylation site"
"potential glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83.1%; Score 1066; DB 21; 99.5%; Pred. No. 1.6e-104;
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                                                                                                                                                                                                                                                                                                                                                Reddy R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                           Tang YT, Hillman JL,
i Y, Yang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ė
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 91; 130pp; English.
                                                                                                                                                                                                                                            99US-0125537.
                                                                                                                                                                                                     22-MAR-2000; 2000WO-US07817.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB90429 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RCGVPFSCCVRDPA 194
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                                                                                                                                                                                                                                                                                                     (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
/note=
                                                                                                                                                                                                                                                                                                                                                              Azimzai Y,
                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-579485/54
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Matches 193; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAA96482.
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                                                                                                                       WO200056891-A2
                                                         Modified-site
                                                                                                                                                                                                                                                               16-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                Yue H, ]
Lu DAM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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nucleotide sequence selected from any of 948 sequences
(ABZ1119-ABZ12066) or their mature protein coding portion, active domain
coding protein or complementary sequences. The polymucleotides are useful
coding protein or complementary sequences. The polymucleotides are useful
for identifying expressed genes or for physical mapping of human genome.
The encoded polypeptides (ABP68902-ABP69849) are useful as molecular
confidentifying expressed genes or for physical mapping of human genome.
The encoded polypeptides (ABP68902-ABP69849) are useful as molecular
confidentifying expressed genes or generating antibodies, in
medical imaging, screening and diagnostic assays and for treating
cell-proliferative disorders (cancer), neurodegenerative diseases
(Parkinson's or Alzheimer's disease), autoimmune diseases (multiple
sclerosis, diabetes, lupus) genetic disorders, myeloid or lymphoid
cdisorders, platelet or coagulation disorders, wound, burns, incision,
ulcers, liver or lung fibrosis, infections (bacterial, viral, fungal,
comparasitio), arrhritis, etc.
Concert The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from NIPO
cat fip.wipo.int/pub/published_pot_sequences.
                                                                                                                                                                                                   Human; genome mapping; gene therapy; food supplement; virus; fungus; cell-proliferative disorder; neurodegenerative disease; bacterial; Parkinson's disease; Alzheimer's disease; autoimmune disease; multiple sclerosis; diabetes; genetic disorder; wound; burn; infection; arthritis; cytostatic; immunomodulator; nootropic; neuroprotective; antiparkinsonian; antidiabetic; immunosuppressive; dermatological; haemostatic; vulnerary; fungicide; antibacterial; virucide; protozoacide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ren F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated polynucleotide (I) comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynucleotides comprising sequences assembled from expressed agequence tags (BSTs), useful for treating cell-proliferative, neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet or coagulation disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhao QA, F
Ghosh M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 9; SEQ ID NO 1646; 1012pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhang J, Zh
R, Wang Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 972.5; DB 23;
Pred. No. 1.3e-94;
1; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Goodrich RW, Asundi V, Zhai
Aa Y, Yamazaki V, Chen R, Wang D, Drmanac RT;
                                         ABP69599 standard; Protein; 330 AA
                                                                                                                                                                 Human polypeptide SEQ ID NO 1646.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 91.9%;
Matches 181; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-MAR-2001; 2001US-0799451
                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ma Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-759812/82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              330 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ABZ11816.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200270539-A2
                                                                                                                                                                                                                                                                                                                                                        antiarthritic.
                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                         20-JAN-2003
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                                                                                ABP69599;
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RESULT 6
                     ABP69599
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AAC97991 to AAC98763 encode the human colon cancer associated proteins, called human colon cancer antigens, given in AAB51234 to AAB54006. The human colon cancer antigens can have cytostatic, cardioactive, muscular; neuroprotective, immunomodulatory, gynaecological, gastrointestinal, vulnerary, nephrotropic, antiinfective and antibacterial activities, and can be used in gene therapy. The colon cancer antigen polymucleotides, proteins and antibodies to the proteins are useful for the prevention, treatment and diagnosis of colon disorders, such as colon cancer. The polymucleotides may be used in diagnostics and research, such as for chromosome identification, and as hybridisation probes. The proteins may also be used to prevent diseases such as neural disorders, immune system disorders, muscular disorders, reproductive disorders, immune gastrointestinal disorders, wounds, renal disorders, infectious diseases, and cardiovascular disorders. AAC98764 to AAC98772 and AAC98707 represent sequences used in the exemplification of the present
                                                                      177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Colon cancer associated gene sequences, referred to as colon cancer antigens, useful for the treatment, prevention, and diagnosis of colon
                                                                    61 LDPVWL--VCGSWRRHVGAGLCWAAIGALRENTFLLKFFSVFLGLIFFLELATGILAFVF
LDPVWLFVVVGGVMSVLGFAGC---IGALRENTFLLKFFSVFLGLIFFLELATGILAFVF
                                                                                                                                                                                                                                                                                                                                                                                                                                          identification; cytostatic; cardioactive; neuroprotective; vulnerary; immunomodulatory; muscular; gynaecological; gastrointestinal; nephrotropic; antiinfective; antibacterial; gene therapy; wound; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; reproductive disorder; gastrointestinal disorder; renal disorder; infectious disease; cardiovascular disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                         cancer; colon cancer antigen; diagnosis; detection;
                                                                                                                                                                                                                                                                                                                                                                                         Human colon cancer antigen protein sequence SEQ ID NO:978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 11; Page 1550-1551; 2104pp; English.
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                                                                                                                                                                  SRERCGVPFSCCVRDPA 195
                                                                                                                                           SRERCGVPFSCCVRDPA 194
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271 AA;

Sequence

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1 MPGKHQHPQEPEVGCCGKYFLFGFNIVFWVLGALFLAIGLMAMGEKGVLSNISALTDLGG 60

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Indels

DB 23; Length 330;

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e.g. arrhythmia and atherosclerosis, cerebrovascular diseases, neural disorders e.g. Alzheimer's and Parkinson's disease, reproductive disorders, skin disorders e.g. psoriasis, renal system disorders e.g. nephritis, (auto)immune system disorders e.g. graft vs. host disease, hyperproliferative disorders e.g. neoplasms of the pancreas, ocular disorders e.g. neoplasms of the pancreas, ocular disorders e.g. neoplasms of the pancreas, ocular disorders e.g. state of the pancreas ocular disorders e.g. neoplasms of the pancreas, ocular disorders e.g. state of the pancreas ocular disorders e.g. state of the pancreas ocular disorders e.g. state of the pancreas ocular disorders e.g. state ocular disorders e.g. state ocular disorders e.g. state ocular disorders e.g. state ocular disorders e.g. state ocular disorders e.g. state ocular disorders e.g. state ocular disorders e.g. state ocular disorders e.g. state ocular disorders e.g. state ocular disorders e.g. state ocular disorders e.g. state ocular disorders e.g. state ocular disorders e.g. state ocular disorders e.g. state ocular disorders e.g. state ocular disorders e.g. state ocular disorders e.g. state ocular disorders e.g. state ocular disorders e.g. state ocular disorders e.g. state ocular disorders e.g. state ocular disorders e.g. state ocular disorders e.g. state ocular disorders e.g. state ocular disorders e.g. state ocular disorders e.g. state ocular disorders e.g. state ocular disorders e.g. state ocular disorders e.g. state ocular disorders e.g. state ocular disorders e.g. state ocular disorders e.g. state ocular disorders e.g. state ocular disorders e.g. state ocular disorders e.g. state ocular disorders e.g. state ocular disorders e.g. state ocular disorders e.g. state ocular disorders e.g. state ocular disorders e.g. state ocular disorders e.g. state ocular disorders e.g. state ocular disorders e.g. state ocular disorders e.g. state ocular disorders e.g. state ocular disorders e.g. state ocular disorders e.g. state ocular disorders e.g. state ocular disorder
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/label= dk329_1 mature protein
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7, Steininger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY42381 standard; Protein; 193 AA.
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                                                                                                                                                                                       61.7%;
72.2%;
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99US-0251600.
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Best Local Similarity 72.29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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Agostino MJ,
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N-PSDB; AAZ20854.
                                                                                                                                                    268 AA;
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signal sequence cl
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17-FEB-1999;
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Treacy M,
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                                                                                                                                                                                                                                       IRDQLNFFINNNVKAYRDDIDLQNLIDFAQEYWSCCGARGPNDWNLNIYFNCTDLNPSRE 180
                                                                                                                                                                                                                                                          Human; 4 transmembrane superfamily receptor protein;
andocrine; carditovascular; cerebrovascular disease; neural disorder;
reproductive; skin; renal system; autoimmune; hyperproliferative; ocular;
bacterial infection; viral; fungal.
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                                                                                        1 MPGKHOHFOEPEVGCCGKYFLFGFNIVFWVLGALFLAIGLWAWGEKGVLSNISALTDLGG
                                                                                                               Isolated nucleic acid molecule encoding human soluble 4 transmembrane superfamily receptor protein, useful for diagnosing, treating and/or preventing disorders e.g. Alzheimer's, cancer and arrhythmia -
                                                         Gaps
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                 Query Match
69.0%; Score 885; DB 21; Length 271;
Best Local Similarity 79.9%; Pred. No. 2e-85;
Matches 155; Conservative 16; Mismatches 21; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB49505 standard; Protein; 268
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99US-0137797.
99US-0138573.
99US-0149447.
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N-PSDB; AAC90015.
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11-JUN-1999;
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CA;
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120
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                                                                            1 MPGKHQHFQEPEVGCCGKYFLFGFNIVFWVLGALFLAIGLWAWGEKGVLSNISALTDLGG
                                                                                                               1 MSGK--HYKGPEVSCCIKYFIFGFNVIFWFLGITFLGIGLWAWNEKGVLSNISSITDLGG
                                                                                                                                                                                                                             IRDOLNFFINNNVKAYRDDIDLQNLIDFAQEYWSCCGARGPNDWNLNIYFNCTDLNPSRE
                                                                                                                                                    LDPVWLFVVVGGVMSVLGFAGCIGALRENTFLLKFFSVFLGLIFFLELATGILAFVFKDW
                                         Gaps
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therapy;
   Length 268;
; Score 791; DB 22; Length 2; Pred. No. 1.8e-75; 16; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ed protein; cDNA library; clone; transmembrane sequence cloning; hybridization cloning; gene
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Lavallie E, Collins-racie LA, Evans C, 7, Steininger RJ, Spaulding V, Wong GG;

McCoy JM, Lavallie E, Agostino MJ, Steining Fechtel K, Merberg D;

WPI; 2001-639363/73.

Clark H,

N-PSDB; AAS59291

(GEMY) GENETICS INST INC.

22-MAR-2001; 2001WO-US09369

11-OCT-2001.

Disclosure; Page 577; 619pp; English.

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Secreted human proteins, useful as vaccine for treating various diseases such as autoimmune disorders (e.g. multiple sclerosis), and nervous system disorders (e.g. stroke)
                                                                                                                             30-MAR-2000; 2000US-0539330.
04-DEC-2000; 2000US-0729674.
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Treacy M.
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                                                                                                                                              The PNB and proteins of the invention are predicted to have biological activities which would make them suitable for treating, preventing or activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, immulating (e.g. as vaccines) or suppressing activity, hemostatic cativity, and thrombolytic activity, tissue growth activity, hemostatic and thrombolytic activity, chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chemotactic/chem
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                                                             This is the amino acid sequence of the dk329_1 protein, which is derived from the dk329_1 clone isolated from a human fetal kidney cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MPGKHQHFQEPEVGCCGKYFLFGFNIVFWVLGALFLAIGLWAWGEKGVLSNISALTDLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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   Claim 13; Page 101-102; 125pp; English.
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Matches 139, Conservative
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The invention relates to novel human secreted proteins, the nucleic acids encoding them. The protein may exhibit cytokine, cell proliferation or cell differentiation activity or may induce production of other or cell differentiation activity which is useful for the treatment of cytokines in certain cell populations and may exhibit immune stimulating or immune deficiencies and disorders e.g. severe combined confirmance disorders e.g. severe combined immune deficiency (SCID), autoimmune disorders including tissue, skin and organ transplantation and in systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation. The proteins are also useful in the treatment of diseases cond disorders including tissue, skin and organ transplantation and in graft-versus-host diseases (GVHD), in the induction of tumour immunity, confirmation or lymphoid cell deficiencies, wound healing and tissue repair, confirmancery processes, diseases of the peripheral nervous system, inflammatory processes, diseases, funtington's disease, inflammatory processes, disease, Huntington's disease, osteoporosis or osteoarthritis, mediated by inflammatory bowel disease, ulcers, bone regeneration. The protein having activities and shy-brager syndrome, infections, infarction of cardiac and central nervous system vessel e.g. stroke, gepsis, inflammatory bowel disease, ulcers, bone regeneration. The contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. The recont second acids are also useful as a food supplements. The recont second acids are also useful as food supplements. The processes are also useful as food supplements.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54.5%; Score 699; DB 22; Length 193; 62.9%; Pred. No. 7.1e-66; ative 16; Mismatches 30; Indels 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 RCGVPFSCCVRDPA-----MSSTPSVAMMSGSNWSWSR 214
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ID ABB5
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Human; clone bd106-7; clone yb8-1; ATCC number 98599; gene therapy; immune disorder; bacterial infection; fungal infection; cancer; tumour; autoimmune disorder; spetemic lupus erythematosus; wound; ulcer; inhibin; osteoporosis; osteoarthritis; nervous system disorder; neuropathy; Alzheimer's disease; Parkinson's disease; Huntington's disease; activin; haemophilia; cardiac infarction; stroke; sepsis; archritis; vulnerary; ischaemia-reperfusion injury; inflammatory bowel disease; chemotactic; cohn's disease; chemotactic; anti-inflammatory; immunomodulator; neuroprotective; haemostatic; thrombolytic; anti-inflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to isolated polynucleotides (ABA90876-ABA90968 and ABA90980) and encoded proteins (ABB55698-ABB55800), especially polynucleotides SEQ ID NO 1 (ABA90876) and SEQ ID NO 19 (ABB95689) and proteins SEQ ID NO 2 (ABB55698) and SEQ ID NO 20 (ABB55707) contained in clones bd306-7 and yb8-1 respectively and the clones bd306-7 and yb8-1 are deposited with the American Type Culture Collection (ATCC) with accession number 98599. The polynucleotides and encoded polypeptides have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        secreted proteins and encoding polynucleotides, useful in gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           therapies, particularly for preventing or treating autoimmune disorders, cancer, graft-versus-host disease, wound, osteoporosis,
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Steininger RJ, Spaulding V;
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4, Agostino MJ,
Fechtel K;
                                                                                         Human polypeptide SEQ ID NO 170.
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97US-067454P.
97US-063749P.
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LAVALLIE E R.
COLLINS-RACIE L A.
                                               14-FEB-2002 (first entry)
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STEININGER R J.
SPAULDING V.
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Clark H, Fe
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N-PSDB; ABA90960.
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FECHTEL K.
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Wong GG,
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ABB55782;
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(EVAN/)
(MERB/)
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(WONG/)
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cytostatic, anti-inflammatory, immunomodusatic, virturaray, interary, currestatic, and anti-inflammatory activity and acting as cytokine modulators, and anti-inflammatory activity and acting as cytokine modulators, haematopoiesis regulators, tissue growth modulators and/or cadherin suppressors. The polypeptides and polymucleotides are useful in gene therapies, particularly for preventing, treating or ameliorating any of the following diseases: immune deficiency and disorders; e.g. bacterial or fungal infections, autoimmune disorders, cancer, systemic lupus erythematosus or graft-versus-host disease; myeloid or lymphoid cell deficiencies; wound, burns, incisions and ulcers, osteoporosis or osteoarthritis, central and peripheral nervous system diseases and neuropathies, e.g. Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis or Shy-Drager syndrome; chaemophilla, cardiac infarction or stroke; inflammations, shock, sepsis or systemic inflammatory response syndrome, ischaemia-reperfusion injury, endotoxin lethality, arthritis, inflammatory bowel disease or crown follows or pemphigus or pemphigus or pemphigus or pemphigus or cancers, pemphigus vulgaris or pemphigus
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               hAemostatic, thrombolytic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rat; gamma-hydroxybutyrate; anti-epileptic; anxiolytic; antineurodegeneration; antipsychotic; brain; dopamine; opioid; GABA; gamma-aminobutyric acid; diagnosis; epilepsy; anxiety; sleep disorder; behavioral disorder; neurodegeneration; Parkinson's disease; psychosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 LDPVWLFVVVGGVMSVLGFAGCIGALRENTFLLKFFSVFLGLIFFLELATGILAFVFKDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MPGKHQHFQEPEVGCCGKYFLFGFNIVFWVLGALFLAIGLWAWGEKGVLSNISALTDLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  30; Indels 36;
                                                                                                                                                                                                                                                                                                                                                                                             Length 193;
immunomodulator, vulnerary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 RCGVPFSCCVRDPA-----MSSTPSVAMMSGSNWSWSSR 214
                                                                                                                                                                                                                                                                                                                                                                                           54.5%; Score 699; DB 23; 62.9%; Pred. No. 7.1e-66; ative 16; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rat gamma-hydroxybutyrate receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABP98695 standard; Protein; 512 AA
cytostatic, anti-inflammatory,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-JUN-2000; 2000WO-FR01687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99FR-0007784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYPA-) UNIV PASTEUR LOUIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 139; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-091570/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Andriamanpandry C,
                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                       Sequence 193 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200078948-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            schizophrenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-DEC-2000.
                                                                                                                                                                                                                                                                                                                    foliaceus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABP98695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   156
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
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Ruben SM, Florence K, Ni J, Rosen CA, Carter KC, Moore PA;
Olsen HS, Shi Y, Young PE, Wei F, Brewer LA, Soppet DR;
                                                                                                                                                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-062296/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAZ65350.
                                                                                                                                                                                                                                 18-MAY-1998;
18-MAY-1998;
18-MAY-1998;
                                                                                                                                                                                                                                                                                                                                       18-MAY-1998;
18-MAY-1998;
WO9958660-A1
                                                                                    06-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lafleur DW,
                                                                                                                                                                                                                                                                                                                                                                                   18-MAY-1998;
                                       18-NOV-1999
                                                                                                                                                                                                                                                                                               18-MAY-1998
                                                                                                                                                                                                           18-MAY-1998
                                                                                                                                                                                                                                                                                                                        18-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Olsen HS
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                                                                                                                                  This sequence represents a novel rat gamma-hydroxybutyrate receptor

(GHBR) isolated from rat brain hypocampal cell cDNA library. The

invention relates to the isolation of this novel sequence, fragments of

it and homologues of the sequence except for those homologues that having

GenBank accession numbers AAC 17120 (human tetraspan NET-4), AA615405,

AA697250 or Af1467230. GHBR is the receptor for gamma-hydroxybutyrate in

the rat brain and is involved in regulating dopaminergic, opioid and

GABA(gamma-aminobutyric acid) ergic activities. The nucleic acid that

encodes the protein is used: (1) as primers or probes for detection and

amplification, particularly for screening gene libraries to identify

promoters and regulators of the GHBR gene; (2) for expression of

recombinant polypeptides; and (3) to detect allelic variants, mutations,

gene (for diagnosing diseases) or susceptibility, associated with

abnormal expression of GHBR). The protein (or cells and transgenic

animals expressing it) is used: (1) to screen for agents that interact

with GHBR; (2) to study expression/activity of the receptor, including

its interaction with other compounds; and (3) to raise antibodies (Ab)

specific for GHBR. The Ab are used to prevent or treat diseases associated

with abnormal expression or activity of GHBR, particularly those

involving cerebral GABA(gamma-aminobutyric acid)ergic and/or dopaminergic

with abnormal from addictive drugs, neurodegeneration (Parkinson's disease),

conversed to prevent or for experimental disease),

withdrawal from addictive drugs, neurodegeneration of hormone (growth

permone and prolactin) that are under dopaminergic control.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGLDPVWLFVVVGGVMSVLGFACCIGALRENTFLLKFFSVFLGLIFFLEATGILAFVFK 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DWIRDQLNFFINNNVKAYRDDIDLQNLIDFAQEYWSCCGARGPNDWNLNIYFN-CTDLNP 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; secreted protein; cancer; tumour; developmental abnormality; foetal deficiency; blood disorder; immune system disorder; inflammation; autoimmune disease; allergy; Alzheimer's disease; cognitive disorder; schizophrenha; arthritis; asthma; psoriasis; sepsis; skin disorder; atherosclerosis; diabetes; cardiovascular disorder; kidney disorder; digestive disorder; endocrine disorder; infection; AlDS; leukaemia; therapy; chromosome 10.
                                     New rat brain gamma-hydroxybutyrate receptor and its encoding nucleic acid, useful for identifying agents for treating e.g. epilepsy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 640.5; DB 22; Length 512;
Pred. No. 3.9e-59;
3; Mismatches 10; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human secreted protein encoded by gene 10 fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY76266 standard; Protein; 270 AA
                                                                                                     Claim 1; Page 62-63; 66pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SRERCGVPFFCWVR 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SRERCGVPFSCCVR 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 89.6'
Matches 120; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           512 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY76266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97
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Endress GA,

98US-0085094. 98US-0085105. 98US-0085180.

99WO-US09847

98US-0085906. 98US-0085920. 98US-0085921. 98US-0085922.

98US-0085923. 98US-0085924. 98US-0085928. 98US-0085925.

98US-0085927

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AA761250 to AA263350 represent 97 isolated human secreted protein genes.

AA776124 to AA77623 are the secreted proteins encoded by the 97 human genes encoding this protein was found to be on chromosome 10.

Genes The gene encoding this protein was found to be on chromosome 10.

The genes and their corresponding secreted polypeptides are 10.

e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 97 genes, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tummours, developmental abnormalities and foetal deficiencies, blood disorders, diseases of the 1 mmune system, autoimmune diseases, inflammation, allergies, Alzheimer's and cognitive disorders, atherosclerosis, diabetes, cardiovascular disorders, kidney disorders, dispetides are also useful for identifying their binding partners.

The secondaries are also useful for identifying their binding partners.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65 WLFVVVGGVMSVLGFAGCIGALRENTFLLKFFSVFLGLIFFLELATGILAFVFKDWIRDQ 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 FREFFESNIKSYRDDIDLONLIDSLOKANQCCGAYGPEDWDLNVYFNCSGASYSREKCGV 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125 LNFFINNNVKAYRDDIDLQNLIDFAQEYWSCCGARGPNDWNLNIYFNCTDLNPSRERCGV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequences shown in AAY76224 to AAY76424 represent fragments of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 YYRYSNAKVSCWYKYLLFSYNIIFWLAGVVPLGVGLWAWSEKGVLSDLTKVTRMHGIDPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 HOHFOEPEVGCCGKYFLFGFNIVFWVLGALFLAIGLWAWGEKGVLSNISALTDLGGLDPV
                   encode,
New isolated human genes and the secreted polypeptides they encoruseful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 49.8%; Score 638.5; DB 21; Length 270; Best Local Similarity 49.4%; Pred. No. 2.9e-59; Matches 119; Conservative 37; Mismatches 66; Indels 19;
                                                                                                                                                                                           Disclosure; Page 428-429; 475pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           270 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   secreted proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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HQHFQEPEVGCCGKYFLFGFNIVFWVLGALFLAIGLWAWGEKGVLSNISALTDLGGLDPV

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The invention relates to novel secreted/transmembrane proteins, and nucleic acids encoding them. The novel proteins are designated TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, TANGO 319, T
----SWSSRAPYTPKAVWAS 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Secreted protein; transmembrane protein; TANGO; human; drug screening; activity modulator; expression modulator; cancer; immunological disorder; cytostatic; immunomodulatory; gene therapy.
                                               183 PFSCCVPDPAQKVVNTQCGYDVRIQLKSKWDESIFTKGCIQALESWLPRNIYIVAGVFIA 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding secreted TANGO and MANGO polypeptides, useful for the prevention, diagnosis and treatment of, e.g. cancers and immune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Barnes TM, Wrighton N, Myers PS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49.8%; Score 638.5; DB 22; Length 270; 49.4%; Pred. No. 2.9e-59; ive 37; Mismatches 66; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human secreted protein TANGO 339, SEQ ID NO:3.
PFSCCVRDPAMSSTPS----VAMMSGSNW---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 9; Page 220-221; 332pp; English.
                                                                                                                                                                                                                                                                                        AAB87034 standard; Protein; 270 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sharp JD, Kirst SJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0365164.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-JUL-2000; 2000WO-US20935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-138647/14.
N-PSDB; AAF90628, AAF90629.
                                                                                                                                                                                                                                                                                                                                                                                                  04-MAY-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     270 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200109162-A2
                                                                                                    226 L 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fraser CC,
Pan Y;
                                                                                                                                                                                                                                                                                                                                                AAB87034;
185
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                                                                                                                                                                                                                                      RESULT 14
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182
                                                               184
                                              65 WLFVVVGGVMSVLGFAGCIGALRENTFLLKFFSVFLGLIFFLELATGILAFVFKDWIRDQ 124
                                                                                                                                                                               PFSCCVRDPAMSSTPS----VAMMSGSNW-----SWSSRAPYTPKAVMAS 225
                                                                                                                                                                                                                183 PFSCCVPDPAQKVVNTQCGYDVRIQLKSKWDESIFTKGCIQALESWLPRNIYIVAGVFIA 242
            62
                                                                                                                                123 FREFFESNIKSYRDDIDLONLIDSLOKANQCCGAYGPEDWDLNVYFNCSGASYSREKCGV
3 YYRYSNAKVSCWYKYLLFSYNIIFWLAGVVFLGVGLWAMSEKGVLSDLTKVTRMHGIDPV
                                                                                                               125 LNFFINNNVKAYRDDIDLQNLIDFAQEYWSCCGARGPNDWNLNIYFNCTDLNPSRERCGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to inhibitors of tetraspan protein, TSPAN-7 which are used to reduce or decrease the expression of TSPAN-7 in a mammalian cell and for treating hyperproliferative disorder, especially cancer in a mammal. The invention also provides TSPAN-7 polypeptides and polymolectides TSPAN-7 inhibitors are useful for inhibiting proliferation of mammalian cells, including tumour cells, for decreasing the side effects of cancer therapy and for treating neoplastic diseases. They are used to modulate TSPAN-7 expression and function in cancer cells, particularly in prostate cancer cells. They are also used in antisense therapy. The present sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; tetraspan protein; TSPAN-7; hyperproliferative disorder;
neoplastic disease; prostate cancer; antisense therapy; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New inhibitor of tetraspan protein useful for reducing the exp
or activities of tetraspan protein in cells, and for treating
hyperproliferative disorder, especially cancer in a mammal
                                                                                                                                                                                                                                                                                                                                                            AAE18535 standard; Protein; 270 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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23; Length 270;

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Indels 19;

Best Local Similarity 49.4% Matches 119; Conservative

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185 PFSCCVRDPAMSSTPS-----VAMMSGSNW------SWSSRAPYTPKAVWAS 225
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Search completed: November 21, 2003, 13:43:36 Job time : 42 secs

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Sequence 2, Application US/09972970

Patent NO. US20020164693A1

GENERAL INFORMATION:

APPLICANT: Shi et al.

TITLE OF INVENTION: TM4SF Receptor Polynucleotides, Polypeptides, and Antibodies
FILE REFERENCE: PT056P1

TOTRENT APPLICATION NUMBER: US/09/972,970

CURRENT FILING DATE: 2001-00-10

PRIOR PAPLICATION NUMBER: PCT/US01/11130

PRIOR PAPLICATION NUMBER: 60/195,336

PRIOR FILING DATE: 2000-04-10

PRIOR FILING DATE: 2000-04-10

NUMBER OF SEQ ID NOS: 8

SOFTWARE: Patentin Ver. 2.0
                                                            Sequence 1, Appli
Sequence 35, Appl
Sequence 205, Appl
Sequence 205, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 116, Appl
Sequence 126, Appl
Sequence 126, Appl
Sequence 126, Appl
Sequence 20, Appl
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Sequence 26, Appl
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US-09-129-674-129

US-09-991-053-15

US-09-991-053-15

US-09-991-053-15

US-09-991-053-15

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US-09-991-053-15

US-09-991-053-18

US-09-991-053-18

US-09-991-053-18

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US-09-991-053-18

US-09-994-271-122

US-10-006-1328-122

US-10-106-138-122

US-10-113-690-277

US-10-173-690-277
US-09-934-268-3

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US-09-934-268-1

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Alignment Scores:
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-Q=Cgn2 1/USPTO spool/USO9972970/runat 21112003 125336_27261/app_query.fasta_1.391
-D==Published Applications NA -OPMT=fastap -SUPFTX-P2D1.rmpb -MINMATCH=0.1
-LOOPEL10 -LOOPEXT=0 -UNITS=bits -START=1 -END--1 -MATRIX=blosund2
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN-0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09972970 @CGN 1 1 221 @runat 21112003 125336_27261
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                                                                                                                               November 21, 2003, 15:29:38 ; Search time 335 Seconds (without alignments) 2273.109 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB_seq:*
3: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB_seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Publication No. US20030096305A1
Publication No. US20030096305A1
Publication No. US20030096305A1
APPLICANT: Meyers, Rachel
APPLICANT: Clucksmann, Maria Alexandra
APPLICANT: Curtis, Rory A. J.
APPLICANT: Bandaru, Rasekhar
APPLICANT: Bandaru, Rasekhar
APPLICANT: Leiby, Kevin R.
TITLE OF INVENTION: NOVEL HUMAN MEMBRANE-ASSOCIATED PROTEIN AND
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Matches:
Conservative:
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                                     3.73e-132
1215.50
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                                                           Percent Similarity:
Best Local Similarity:
  Homo
                                Alignment Scores:
Pred. No.:
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US-10-162-435-37
 , ORGANISM: Hc
US-09-934-268-3
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US-09-934-268-3
i Sequence 3, Application US/09934268
i Sequence 3, Application US/09934268
i Sequence 3, Application US/09934268
i Sequence 3, Application US/09934268
i GENERAL INFORMATION:
I TILE OF INVENTION: MEMBER AND USES THEREOF
I TILE OF INVENTION: MEMBER AND USES THEREOF
i TILE OF INVENTION: MEMBER: US/09/001
i CURRENT PILING DATE: 2001-08-21
i PRIOR APPLICATION NUMBER: 60/226,612
i PRIOR APPLICATION NUMBER: 60/226,612
i PRIOR PILING DATE: 2000-08-21
i NUMBER OF SEQ ID NOS: 4
i SEQ ID NOS: 4
i SEQ ID NOS: 4
i LENGTH: 813
i TYPE: DNA
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Conservative:
Mismatches:
Indels:
Gaps:
                                                  US-09-972-970-4 (1-233) x US-09-972-970-2 (1-2538)
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Percent Similarity:
Best Local Similarity:
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                                                                                                                       GlyLeullePhePheLeuGluLeuAlaThrGly1leLeuAlaPheValPheLysAspTrp
                                                                   241 GGCTGCATTGGGGCCCTCCGGGAGAACACCTTCCTGCTCCAAGTTTTTCTCCGTGTTCCTC
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                                       GlyCys1leGlyAlaLeuArgGluAsnThrPheLeuLeuLysPhePheSerValPheLeu
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OTHER INFORMATION: Incyte ID No. US20030190640A1 234056.5
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GENERAL INFORMATION:
APPLICANT: Faris, Mary
APPLICANT: Faris, Mary
TITLE OF INVENTION GENES EXPRESSED IN PROSTATE CANCER
FILE REPERENCE: PA-0027-1 US
CURRENT APPLICATION NUMBER: US/10/252,157
CURRENT PILING DATE: 2002-10-01
FRIOR FILING DATE: 2001-05-31
NUMBER OF SEQ ID NOS: 501
SOFTWARE: PERL PROGRAM
SEQ ID NO 153
LENGTH: 2461
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Publication No. US20030190640A1
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US-10-252-157-153
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US-10-252-157-153
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TITLE OF INVENTION: CELL SURFACE PROTEIN FAMILY MEMBERS
CURRENT FILING DATE: 10448-189001
CURRENT FILING DATE: 2002-06-04
PRIOR PAPLICATION NUMBER: US 09/836,499
PRIOR PILING DATE: 2001-04-17
PRIOR PILING DATE: 2001-04-17
PRIOR PILING DATE: 2001-04-18
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2001-06-25
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 37
LENGTH: 813
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; ORGANISM: Homo sapiens
US-10-162-435-37
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                                                                                                                                                    41 TrpAlaTrpGlyGluLysGlyValLeuSerAsnIleSerAlaLeuThrAspLeuGlyGly
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APPLICANT Glucksmann, Maria Alexandra
APPLICANT Curlis, Rory A. J.
APPLICANT Curlis, Rory A. J.
APPLICANT Expeller-Libermann, Rosana
APPLICANT Bandaru, Rajasekhar
APPLICANT Bandaru, Rajasekhar
APPLICANT Bandaru, Rajasekhar
APPLICANT BANDARION: NOVEL HUMAN MEMBRANE-ASSOCIATED PROTEIN AND
TITLE OF INVENTION: NOVEL HUMAN MEMBRANE-ASSOCIATED PROTEIN AND
TITLE OF INVENTION: CELL SURFACE PROTEIN FAMILY MEMBERS
TILE REFERENCE: 10448-189999
PRIOR PLILING DATE: 2001-04-17
PRIOR APPLICATION NUMBER: DCT/USO1/12420
PRIOR PLILING DATE: 2001-04-17
PRIOR PLILING DATE: 2001-04-17
PRIOR FILING DATE: 2000-04-18
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                 US-09-972-970-4 (1-233) x US-09-934-268-1 (1-3184)
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US-10-162-435-35
IS-10-162-435-35
Sequence 35. Application US/10162435
Publication No. US20030096305A1
GENERAL INFORMATION:
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                           41 TrpAlaTrpGlyGluLysGlyValLeuSerAsnIleSerAlaLeuThrAspLeuGlyGly
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Patent No. US20020172986A1
GENERAL INFORMATION:
TITLE OF INVENTION: 23228, A NOVEL HUMAN TETRASPANIN FAMILY
TITLE OF INVENTION: MEMBER AND USES THEREOF
FILE REFERENCE: 10448-079001
CURRENT APPLICATION NUMBER: US/09/934,268
CURRENT FILING DATE: 2001-08-21
PRIOR FILING DATE: 2000-08-21
PRIOR FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FABLES OF VALIDAM WINDER: SEQ ID NO 1
SEQ ID NO 1
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US-09-934-268-1
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ORGANISM: Homo sapiens
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Best Local Similarity:
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NAME/KEY: CDS
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Pred. No.:
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US-09-934-268-1
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TITLE OF INVENTION: THASF Polynucleotides, Polypeptides, and Antibodies FILE PREPERENCE: PTOORBEL
CURRENT APPLICATION NUMBER: US/10/103,196
CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: US/10/13504
PRIOR FILING DATE: 2000-11-36
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: PCT/US00/13504
PRIOR FILING DATE: 2000-01-28
PRIOR FILING DATE: 2000-01-28
PRIOR FILING DATE: 1999-08-18
PRIOR APPLICATION NUMBER: 60/149,447
PRIOR FILING DATE: 1999-06-11
PRIOR FILING DATE: 1999-06-11
PRIOR APPLICATION NUMBER: 60/130,573
PRIOR FILING DATE: 1999-06-11
PRIOR FILING DATE: 1999-06-11
PRIOR FILING DATE: 1999-06-03
PRIOR FILING DATE: 1999-06-03
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                     468 GGTCTCATCTTCTTCCTGGAGCTGGCAACAGGGATCCTGGCCTTTGTCTTCAAGGACTGG 527
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                                                            157 ArgecedecaAgeaceagearrrecaggaacergaggregergergegaaaraerre
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Matches:
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ORGANISM: Homo sapiens
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Best Local Similarity:
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US-10-103-196-4
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Matches:
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PRIOR APPLICATION NUMBER: US 09/891,008
PRIOR FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: US CVT/US01/19963
PRIOR APPLICATION NUMBER: US 00/214,220
PRIOR APPLICATION NUMBER: US 09/860,868
PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 2001-05-18
PRIOR PRIOR DATE: 2001-05-18
PRIOR APPLICATION NUMBER: US 09/860,868
PRIOR PILING DATE: 2001-05-18
PRIOR PILING DATE: 2001-05-19
PRIOR PILING DATE: 2001-06-21
PRIOR PILING DATE: 2001-06-21
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PRIOR PILING DATE: 2001-06-3
PRIOR PILING DATE: 2001-06-3
PRIOR PILING DATE: 2001-01-08
PRIOR PILING DATE: 2002-01-08
PRIOR PILING DATE: 2001-01-08
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US-10-162-435-35
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ORGANISM: Homo sapiens
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Publication No. US20030040617A9;
GENERAL INFORMATION:
APPLICANT: Rosen et al.
ITILE OF INVENTION: Nucleic Acids, Proteins and Antibodies
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180
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 NAME/KEY: misc feature
LOCATION: (1623)
OTHER INFORMATION: n.equals a,t,g,
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958.50
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74.71%
                                                                 ; OTHER INFORMATION: n equals US-09-925-299-205
                                       NAME/KEY: misc feature LOCATION: (1643)
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Best Local Similarity:
Query Match:
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US-09-925-299-205
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GGTCTCATCTTCTTCCTGGAGCTGGCAACAGGGATCCTGGCCTTTGTCTTCAAGGACTGG
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APPLICANT: ROSE et al.; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies; TILE OF INVENTION Nucleic US/09/925,299; CURRENT APPLICATION NUMBER: US/09/925,299; CURRENT FILING DATE: 2001-08-10; PRIOR APPLICATION NUMBER: PCT/US00/05883; PRIOR FILING DATE: 2000-03-08; PRIOR APPLICATION NUMBER: 60/124,270; NUMBER OF SEQ ID NOS: 1556; SOFTWARE: PatentIn Ver. 2.0; SEQ ID NO 205; LENGTH: 1655
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ORGANISM: Homo sapiens
PRATURE:
NAME/KEY: misc feature
LOCATION: (1548)
OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc feature
LOCATION: (1559)
OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc feature
LOCATION: (1564)
OTHER INFORMATION: n equals a,t,g, or
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US-09-925-299-205
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Sequence 5, Application US/10103196

Sequence 5, Application US/10103196

Bublication No. US20030050466A1

GENERAL INFORMATION:

APPLICATONT: Ni et al.

TILE OF INVENTION: TW4SF Polynucleotides, Polypeptides, and Antibodies

FILE REFERENCE: PT008P1

CURRENT FILING DATE: 2002-03-22

PRIOR PPLING DATE: 2000-11-08

PRIOR PLING DATE: 2000-11-08

PRIOR APPLICATION NUMBER: 60/178,770

PRIOR PLING DATE: 2000-05-18

PRIOR PLING DATE: 2000-06-18

PRIOR PPLING DATE: 1099-06-11

PRIOR PLING DATE: 1999-06-01

PRIOR PLING DATE: 1999-06-01

PRIOR PLING DATE: 1999-05-19

PRIOR PLING DATE: 1999-05-19

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PRIOR PLING DATE: 1999-05-19
       871 CAGTGTGGCTATGATGCCAGGCAAAACCAGAAGTTGACCAGCAGATTGTAATCTACACG 930
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                                                                                 ArgCysGlyValProPheSerCysCysValArgAspProAla----MetSerSerThrPr
                                                                                                   Met ProGlytysHisGlnHisPheGlnGluProGluValGlyCysCysGlyLysTyPhe
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ORGANISM: Homo sapiens
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OTHER INFORMATION:
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US-10-103-196-5
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Conservative:
Mismatches:
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FILE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT APPLICATION NUMBER: US/09/925,299
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: PatentIn Ver: 2.0
SENGTH: 1655
                                                                                                                                                                                                                                PEATURE:
NAME/KEY: misc feature
LOCATION: (1548)
COTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (1559)
COTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (1564)
COTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (1623)
COTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (1633)
COCATION: (1643)
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ORGANISM: Homo sapiens
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Best Local Similarity:
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; Sequence 10, Application US/10103196
; Sequence 10, Application US/10103196
; Bublication No. US20030050466A1
; GENERAL INFORMATION:
    APPLICANT: Ni et al.
; TITLE OF INVENTION: TH4SF Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: P7008P1
; CURRENT APPLICATION NUMBER: US/10/103,196
; PRIOR PILING DATE: 2002-03-22
; PRIOR PAPLICATION NUMBER: 60/707,936
; PRIOR PILING DATE: 2000-01-08
; PRIOR PILING DATE: 2000-01-28
; PRIOR PILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/178,770
; PRIOR PILING DATE: 1999-08-18
; PRIOR PILING DATE: 1999-08-18
; PRIOR PILING DATE: 1999-06-01
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                      LeuAspProValTrpLeuPheValValGlyGlyGlyValMetSerValLeuGlyPheAla
                                                                             GlyCysIleGlyAlaLeuArgGluAsnThrPheLeuLeuLyBPhePheSerValPheLeu
                                                                                                                              pileArgAspGlnLeuAsnPhePheIleAsnAsnAsnValLysAlaTyrArgAspAspIl
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; ORGANISM: Homo sapiens
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Mismatches:
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Patent No. US2001003935A1
GENERAL INFORMATION:
APPLICANT: McCoy, John M.
APPLICANT: Lavallie, Edward R.
APPLICANT: Collins-Racie, Lisa A.
APPLICANT: Evans, Cheryl
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Treacy, Maurice
Agostino, Michael J.
Steininger II, Robert J.
Spaulding, Vikki
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82.70%
75.53%
69.56%
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APPLICANT: Wong, Gordon G.
APPLICANT: Clark, Hilary
APPLICANT: Clark, Hilary
APPLICANT: Fechtel, Kim
APPLICANT: Fechtel, Kim
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION'S SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: 6055-64
CURRENT FAPLICATION NUMBER: US/09/729,674
CURRENT FILING DATE: 2000-12-04
PRIOR PAPLICATION NUMBER: 09/539,330
PRIOR PILING DATE: 2000-3-30
NUMBER OF SEQ ID NOS: 283
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 169
LENGTH: 1110
                                                                                                                                                                                                                                                                                                                                                                                    290 TGGGCATGGAATGAAAAGGAGTTCTGTCCAACATCTCTTCCATCACCATCTCGGCGGC 349
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Matches:
Conservative:
Mismatches:
Indels:
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807.00
76.50%
69.66%
62.90%
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US-09-729-674-169
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Best Local Similarity:
Query Match:
DB:
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APPLICANT: Steininger II, Robert J.
APPLICANT: Steininger II, Robert J.
APPLICANT: Bowman, Michael R.
APPLICANT: Bowman, Michael R.
APPLICANT: Gradung, Vikki
APPLICANT: Clark, Hilary
APPLICANT: Remick, Richard J.
APPLICANT: Remick, Richard J.
APPLICANT: Grabam, James R. Kamalakar
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APPLICANT: Grabam, James 
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                                                                                                                                                                                       Sequence 126, Application US/09822846 Publication No. US20030027139A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                           APPLICANT: Jacobs, Kenneth
APPLICANT: MCCOY, JOHN M.
BAPLICANT: LaVallie, Edward R.
APPLICANT: Collins-Racie, Lisa
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Treacy, Maurice
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; ORGANISM: Homo sapiens
US-09-822-846-126
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IleArgAspGlnLeuAsnPhePheIleAsnAsnAsnValLysAlaTyrArgAspAspIle
                                                                         HisGlnHisPheGlnGluProGluValGlyCy8Cy8GlyLysTyrPheLeuPheGlyPhe
                                                                                                                                          762 GATTTGCAAAACCTCATAGACTTCACCCAGGAATATTGGCAGTGCTGTGGGCTTTTTGGA
                                                                                                                 141 AspLeuGlnAsnLeuIleAspPheAlaGlnGluTyrTrpSerCysCysGlyAlaArgGly
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US-09-905-674-1
; Sequence 1, Application US/09905674
; Publication No. US20030039647A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Garcia, Pablo
; TITLE OF INVENTION: TETRASPAN PROTEIN AND USES THEREOF
; FILE REFERENCE: PP-01700.002/200130.521
; CURRENT APPLICATION NUMBER: US/09/905,674
; CURRENT FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 1
; SEQ ID NO 1
; LENGTH 1388
                                                                                                                                                                       161 ProAsnAspTrpAsnLeuAsnIleTyrPheAsnCysThrAsp 174
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Mismatches:
Indels:
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Matches:
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| LOCATION: 1377
| OTHER INFORMATION: n = A.T.C or G
| LOCATION: n = A.T.C or G
| LOCATION: n = A.T.C or G
| CATION: 1285, 1377
| OTHER INFORMATION: n = A.T.C or G
| US-09-905-674-1
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ORGANISM: Homo sapiens
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CAAAACCTCATAGACTTCACCCAGGAATATTGGCAGTGCTGTGGGGCCTTTTGGAGCTGAT
                           GlyvalProPheSerCysCysValArgAspProAla----MetSerSerThrProSerVa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: NET-4 oligonucleotide used in cell proliferation OTHER INFORMATION: assay on SW620 cells
                                                                                                                                                                                                                                                                                                                APPLICANT: Reinhard, Christoph
APPLICANT: Jefferson, Anne B.
APPLICANT: Jefferson, Anne B.
APPLICANT: Winter, Jill A.
APPLICANT: Winter, Jill A.
APPLICANT: Winter, Jill A.
APPLICANT: Winter, Jill A.
APPLICANT: Winter, Jill A.
APPLICANT: Winter, Jill A.
APPLICANT: Winter, Jill A.
APPLICANT: Winter, Jill A.
APPLICANT: Winter, Jill A.
APPLICANT: Randazzo, Filippo
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: NOPPLASTIC DISEASE USING NET-4 MODULATORS
FILE REFERENCE: PP-01701.002/200130.522
CURRENT FILING DATE: 2001-06-05
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 864
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Matches:
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61.57%
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               733 CAGGCGCTGGAAAGCTGGCTCCCGGGAACA 763
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US-09-016-444-938
US-08-807-044-938
US-08-2016-228-2
US-08-108-228-3
US-08-108-228-3
US-08-108-228-3
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US-09-482-273-41
    TYPE: DNA ORGANISM: Homo sapiens
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1 MPGKHQHFQEPEVGCCGKYF......RAPYTPKAVWASLRSGCRTT 233
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2: /cgn2 6/ptodata/1/ina/5B COMB.seq:*
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5: /cgn2 6/ptodata/1/ina/6B COMB.seq:*
5: /cgn2 6/ptodata/1/ina/PCTUS COMB.seq:*
6: /cgn2 6/ptodata/1/ina/backfles1.seq:*
                      GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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US-09-188-930-643
US-09-312-283C-62
US-09-313-599-5
US-09-333-599-1
US-09-333-599-1
US-08-705-771-8
US-08-807-044-4
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CURRENT APPLICATION NUMBER: US/09/188,930A	Qy 11 ProGluValGlyCysCysGlyLysTyrPheLeuPheGlyPheAsnIleValPheTrpVal 30 CCTGAAGTCAGTGTTGTTGCATCAATACTTCTTTTTGGCTTCAATGTCATATTTTGGTTT 66 Qy 31 LeuGlyAlaLeuPheLeuAlaileGlyLeuTrpAlaTrpGlyGluLySGlYValLeuSer 50 Db 67 TTGGGAATAACGTTTCTTGGAATCGGACTGGGGCTGGAATGAAAAAGTCTCTCTC	127 71 187 79 247 81 307 99	S S S S S S S S S S S S S S S S S S S	1 TrE: Mouse
Score	Oy 63 ProValTrpLeuPheValValValGlyClyValMetSerValLeuGlyPheAlaGlyCy8 82	123 AppGlnLeudsnPhePheIleAsnAsnashIvsalaTyrargAspAspIleAspLeu 123 AppGlnLeudsnPhePheIleAsnAsnashIvsalaTyrargAspAspIleAspLeu 1469 GGGAAGTGGGATGCGATGGCATTGGCATGCGATGGCATTGGATCTG 143 GlnAsnLeulleAppheAlaGlnGluTyrTrpSerCysCysGlyAlaArgGlyProAsn 147 GlnAsnLeulleAppheAlaGlnGluTyrTrpSerCysCysGlyAlaArgGlyProAsn 1529 CAGAACTCATTGATTTTGGCCAGAAAAGTTTAGCTGCTGTGGAGGGATTTCCTACAG 163 AspTrpAsnLeuAsnIleTyrPheAsnCysThrAspLeuAsnProSerArgGluArgCys 161	QY 194	<pre>; APPLICANT: Onrust, Rene ; APPLICANT: MAXISON, James Grag ; TITLE OF INVENTION: Compositions Isolated From Skin Cells ; TITLE OF INVENTION: and Methods For Their Use ; FILE REFERENCE: 11000.1011c1 ;</pre>

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187 GCCAGCCCGAGCCTGAGCTCTGTCAATGACATCCAAGGAGAAATGAGGTTAATGAGAGA 246
                                                                                                                                                                              247 CATTAATTAAACACTCCCTCACCCCACCGCACCAAACCAGTTGGGTTCTTCTGATATTCT 306
                             LeuGlyAlaLeuPheLeuAlaIleGlyLeuTrpAlaTrpGlyGluLysGlyValLeuSer
                                                                                                            71 -------GlyGlyValMetSerValLeuGly------
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                                                                                                           11 ProGluvalGlyCysCysGlyLysTyrPheLeuPheGlyPheAsnIleValPheTrpVal
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Batent No. 6573095

GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onruse, Rene
APPLICANT: Convert, Rene
APPLICANT: Onruse, Rene
APPLICANT: Onruse, Rene
APPLICANT: Muxison, James G.
APPLICANT: Muxison, James G.
APPLICANT: Muxison, James G.
APPLICANT: Mumble, Krishanand D.
TITLE OF INVENTION: Compositions isolated from Skin Cell
TITLE OF INVENTION: Compositions isolated from Skin Cell
TITLE OF INVENTION: and Methods for Their Use
FILE REFERENCE: 11000.1011c2
CURRENT APPLICANTON NUMBER: US/09/312,283C

CURRENT FILING DATE: 1999-05-14

NUMBER OF SEQ ID NOS: 425

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 62
LENGTH: 399
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           Conservative:
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; Sequence 245 Application US/09312283C
; Patent No. 657305
; GENERAL INFORMATION:
    APPLICANT: Watson, James D.
    APPLICANT: Steaman, Matthew
    APPLICANT: Steaman, Matthew
    APPLICANT: Murison, James G.
    APPLICANT:
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Db 187 GCCAGCCCGAGCCTGAGCTCTCAATGACAATCAAGGAAAATGAGGTTAATGAGAGA 246 Qy 79	Alignment Scores:

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us-09-972-970-4.p2n.rn1

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Parent No. 6498014

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Guigley, James P.
APPLICANT: Geandel, Marco
TITLE OF INVENTION: MONOCLONAL ANTIBOIDES THAT RECOGNIZE ANTIGENS
TITLE OF INVENTION: MONOCLONAL MITH TUMOR METASTASIS
FILE REFERENCE: SUNY
CURRENT FILING DATE: 2000-02-08
PRIOR APPLICATION NUMBER: 09/333,599
PRIOR FILING DATE: 1999-06-15
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ORGANISM: Homo sapiens
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SEQ ID NO 1
LENGTH: 870
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CTCAAGAGT-----GACTACATCAGCCTGCTGGCCTCAGGCACCTACCTGGCCACAGCC 239
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Fatent No. 645898

GENERAL INFORMATION:

APPLICANT: Testa, Jacqueline E.

APPLICANT: Quigley, James P.

APPLICANT: Quigley, James P.

TITLE OF INVENTION: ASSOCIATED WITH TUMOR METASTASIS

TITLE OF INVENTION: ASSOCIATED WITH TUMOR METASTASIS

TITLE OF INVENTION: 1999-06-15

CURRENT APPLICATION NUMBER: US/09/333,599

CURRENT FILING DATE: 1999-06-15

NUMBER OF SEQ ID NOS: 5

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO.1
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ORGANISM: Homo sapiens
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Patent No. 6054289
GENERAL INFORMATION:
APPLICANT: Faul Moore, Reiner Gentz, Hongjin Ji,
APPLICANT: Jian Ni and Jing-Shan Hu
TITLE OF INVENTION: Human Genes, Sequences and
TITLE OF INVENTION: Expression Products
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                              Alignment Scores
US-09-499-781-1
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243 CTGGCCGCACAACAGGGGAGCTTTGCCACGCTGTCCTCT------TCCTTC 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99 PheLeuGlyLeullePhePheLeuGluLeuAlaThrGlylleLeuAlaPheValPheLys 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     137 ArgAspAspIleAspLeuGlnAsnLeuIleAspPheAlaGlnGluTyrTrpSerCysCys 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PheGlyPheAsnIleValPheTrpValLeuGlyAlaLeuPheLeuAlaIleGlyLeuTrp 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42 AlaTrpGlyGluLysGlyValLeuSerAsnIleSerAlaLeuThrAspLeuGlyGlyLeu 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GACAAGATTGACAGGTATGCCCAGCAAGAACTTGAAGAAAGGCTTGCACCTGTACGGCACG 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------LysTyrPheLeu 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79 PhealaGlyCysIleGlyAlaLeuArgGluAsnThrPheLeuLeuLysPhePheSerVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 AspProValTrp-----LeuPheValValValGlyGlyValMetSerValLeuGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108 crecrecrecrecrecrecrecaecaccarcecarcererrerrescenaeae
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66
37
84
84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSER: CARELLA, BYNE, BAIN, GILFILLAN, ADDRESSER: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
CITY: NOSELAND
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                       325800-346 (PF196)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-972-970-4 (1-233) x US-08-705-771-8 (1-1344)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels:
                                                                                                                                                                                                       MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: 18M PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/705,771
FILING DATE: August 30, 1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAMME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
TELEPHONE: 973-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.93e-17
249.50
44.98%
28.82%
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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1344 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19.45$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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Best Local Similarity:
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Pred. No.:
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DB:
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                                                                                                          96 PheSerValPheLeuGlyLeuIlePhePheLeuGluLeuAlaThrGlyIleLeuAlaPhe 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 ValPheLysAspTrpIleArgAspGlnLeuAsnPhePheIleAsnAsnAsnValLysAla 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     136 TyrArgAspAspIleAspLeuGlnAsnLeuIleAspPheAlaGlnGluTyrTrpSerCys 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 156 CysGlyAlaArgGlyProAsnAspTrpAsnLeuAsnIleTyrPheAsnCysThrAspLeu 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |||||||
506 TGTGGTATAAATGGCACGAGTGATTGGACCAGTGGCCCACCACCATCTTGC------ 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----ArgGluArg-CysGly---ValPr 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39 GlyLeuTrp-----AlaTrpGlyGluLysGlyValLeu---SerAsnIleSerAlaLeu 55
                                                                             1 MetProGlyLysHisGlnHisPheGlnGluProGluValGlyCysCysGly-----Lys 18
                                                                                                                                                                               19 TyrPheLeuPheGlyPheAsnIleValPheTrpValLeuGlyAlaLeuPheLeuAlaIle 38
                                                                                                                                                                                                                                                                                                                                                                               ThrAspLeuGlyGlyLeuAspProValTrpLeuPheValValValGlyGlyValMetSer 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76 valLeuGlyPheAlaglyCysIleglyAlaLeuArgGluAsnThrPheLeuLeuLysPhe 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Seed, Brian
APPLICANT: Allen, Janet
APPLICANT: Allen, Janet
APPLICANT: Camerini, David
APPLICANT: Camerini, David
APPLICANT: Gamerini, David
APPLICANT: Stamentsovic, Ivan
APPLICANT: Stamentsovic, Ivan
APPLICANT: Stengelin, Siegfried
APPLICANT: Stengelin, Siegfried
APPLICANT: Amiot, Martine
APPLICANT: Amiot, Martine
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APPLICANT: Stengelin, Siegfried
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APPLICANT: Stengelin, Siegfried
APPLICANT: Stengelin, Siegfried
APPLICANT: Amiot, Martine
APPLICANT: Stengelin, Siegfried
APPLICANT: Amiot Martine
APPLICANT: Stengelin, Siegfried
APPLICANT: Colorado
CONRESPONDENCE ADDRESS:
ADDRESSER: Greenlee & Associates
STATE: Colorado
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                            US-09-972-970-4 (1-233) x US-08-807-044-4 (1-1452)
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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GlyAlaArgGlyProAsnAspTrpAsnLeuAsnIleTyrPheAsnCysThrAspLeuAsn 176
                                                                                                                                                                        177 ProSerArgGluArgCysGlyValProPheSerCysCys------- 189
                                                                                                                                                                                                                                                                          190 ---ValArgAspProAlaMet-----SerSerThrProSerValAlaMetMetSer 205
                                                                                                                                                                                                                                                                                                      627 GCCACGCGG-----GTACCTGACTCCTGCTGCTTGGAGTTCAGTGAGAGCTGT 674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Hilman, Jennifer L.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN TRANSMEMBRANE 4 SUPERFAMILY
WUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1452
67
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: F885EG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/807,044
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Baps:
                                                                                                                                                                                                                                                                                                                                                                          Gly-SerAsnTrpSerTrpSerSer 213
                                                                                                                                                                                                                                                                                                                                                                                                         |||| ::: |||
735 GGAGAACTGCTGGCTGTGGGCATCT 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08807044 Patent No. 5863735 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-055
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COmpatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.75e-17
248.00
48.39%
30.88%
19.33%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 1452 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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Best Local Similarity:
Query Match:
DB:
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LIBRARY: General
Ture: 180140
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STATE: CA
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Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
US-08-807-044-4
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       386 GTATATGAACAGAAGCTGAATGAGTATGTGGCTAAGGGTCTGACCGACAGCATCCACCGT 445
                                                                                                                                                                                                         18 LysTyrPheLeuPheGlyPheAsnIleValPheTrpValLeuGlyAlaLeuPheLeuAla 37
                                                                                                                                                                                  176 AsnProSer-----ValPr
                                                                         APPLICANT: Dong, Jin-Tang, Barrett,
APPLICANT: Dong, Jin-Tang, Barrett,
TITLE OF INVENTION: DIAGNOSTIC METHODS AND
TITLE OF INVENTION: GENE THERAPY USING REAGENTS DERIVED FROM THE
TITLE OF INVENTION: HUMAN METASTASIS SUPPRESSOR GENE KAII
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
                                                                                                                                                506 ididdiaraardddacgacgagidariddaccagrggcccaccagcarcridd----
                                                                                                                                                                                                                                                                            185 oPheSerCysValArgAspProAlaMetSerSerThrProSerVal 201
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74
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFRENCE/DOCKET NUMBER: 2026-4172
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: FLOPPY DISK
COMPUTER: IEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
FILING DATE: 28-APR-1995
                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 19, Application US/08430225A; Patent No. 6204000; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 421792
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.6e-17
248.00
46.67%
30.83%
19.33%
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CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1624 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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                                                                                                                                                                                                                                                                                                                                                    US-08-430-225A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY:
US-08-430-225A-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                           136
                                                                                                              156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TICTICATCCTGCTGCTGATATCCTCCTTGCTGAGGTGACCTTGGCCATCCTGCTCTTT 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ValPheLysAspTrpIleArgAspGlnLeuAsnPhePheIleAsnAsnAsnValLysAla 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TyrPheLeuPheGlyPheAsnIleValPheTrpValLeuGlyAlaLeuPheLeuAlaIle 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ThrAspleuGlyGlyLeuAspProvalTrpLeuPhevalvalvalGlyGlyValMetSer 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlyLeuTrp-----AlaTrpGlyGluLysGlyValLeu---SerAsnIleSerAlaLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1452
67
38
81
31
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
                                         CURRENT APPLICATION DATA:

PAPLICATION NUMBER: PCT/US91/04986
FILING DATE: 19910715
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/553,759
FILING DATE: 13-JUL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/498,809
FILING DATE: 23-MAR-1990
PRIOR APPLICATION NUMBER: US 07/379,076
FILING DATE: 13-JUL-1989
PRIOR APPLICATION NUMBER: US 07/160,416
FILING DATE: 25-FEB-1988
APPLICATION NUMBER: US 07/160,416
FILING DATE: 25-FEB-1988
APPLICATION NUMBER: US 07/160,416
FILING DATE: 25-FEB-1988
APPLICATION NUMBER: US 07/160,416
FILING DATE: 25-FEB-1988
APPLICATION NUMBER: US 07/160,416
FILING DATE: 30-499-8080
TELEPHONE: 303-499-8089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 303-499-8089
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1452 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.75e-17
248.00
48.39%
30.88%
19.33%
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                          598 GCTCAGGTGAAGTGCTGCGGC------TGG------GTCAGCTTCTAC 633
                                                                                                                                                                                                                                                                                                                                                                                                                     AsnCysThrAsp------LeuAsnProSerArgGluArgCysGlyValProPhe 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              198 ThrProSerValAlaMetMetSerGlySer-----AsnTrpSerTrpSerSerArg 214
AAATACTTTCTCTTCCTCTTCAACTTGATCTTCTTTATCCTGGGGGGGAGTGATCCTGGGC 252
                                                                                    73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SerCysCysValArg-----sapProAlaMetSer-----Ser 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   215 AlaProTyr-ThrProLysAlaValTrpAlaSerLeuArgSerGlyCysArgThrThr 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        253 TTCGGGGTGTGGATCCTGGCCGACAGAGCAGTTTCATCTCTGTCCTGCAAACCTCCTCC
                                                                                 AlaLeuThrAspLeuGlyGlyLeuAspProValTrpLeuPheValValValGlyGlyVal
                                                                                                                                     94 LysPhePheSerValPheLeuGlyLeuIlePhePheLeuGluLeuAlaThrGlyIleLeu
                                                                                                                                                                                                                GGGCTGTACTTTGCTTGCTTGCTCGATCCTCATTGCCCAGGTGACGGCCGGGGCCCTC
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181 TTCTACTTCAACATGGGCAAGCTGAAGCAGGAGTGGGCGGCATCGTGACTGAGCTCATT
                                                                                                                                                                                                                                                                                                                          634 AACTGGACAGACAACGCTGAGCTCATGAAT -----CGCCCTGAGGTCACCTACCCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----GlyValLeuSerAsnIleSer
                                                                                                                                                                                                                                                   114 AlaPheValPheLysAspTrpIleArgAspGlnLeuAsnPhePheIleAsnAsnAsnVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
APPLICANT: Guegler, Karl J.
TITLE OF INVENTION: NEW TRANSMEMBRANE PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
SOFRWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/855,140
CLASSIFICATION: 435
                           38 IleGlyLeuTrpAlaTrpGlyGluLys-
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Patent No. 5854022
GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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US-08-855-140-2
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314 ATGGTGACGGCTTCCTCGGCTGCCTGGGGCCATCAAGGAAAACAAGTGCCTCCTCC 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35 PheLeuAlaIleGlyLeuTrpAlaTrpGlyGluLysGlyValLeuSerAsnIleSerAla 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55 LeuThrAspLeuGlyGlyLeuAspProValTrpLeuPheValValValGlyGlyValMet 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75 SerValLeuGlyPheAlaGlyCysIleGlyAlaLeuArgGluAsnThrPheLeuLeuLys 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        115 PheValPheLysAspTrpIleArgAspGlnLeuAsnPhePheIleAsnAsnAsnValLys 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             494 CTGTACCACACCGAGAACAACGTGGGGCTGAAGAACGCCTGGAACATCATCCAGGCTGAG 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 153 TrpSerCysCysGlyAlaArgGlyProAsnAspTrpAsnLeuAsnIleTyrPheAsnCys 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        173 ThrAspLeuAsnProSerArgGluArgCysGlyValProPheSerCysCysValArgAsp 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProAlaMetSerSerThrProSerValAlaMetMetSerGlySerAsnTrpSerTrpSer 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               135 AlaTyr----ArgAspAspIleAspLeuGlnAsnLeuIleAspPheAlaGlnGluTyr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               554 ATGCGATGCTGTGTCACTGACTACAGACTGG------
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60
30
92
36
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
                                                                                    NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0296
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPAX: 415-845-4166
                                                               ATTORNEY/AGENT INFORMATION: NAME: Billings, Lucy J.
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41.28%
27.52%
18.08%
                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 977 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                      TELEX:
INFORMATION FOR SEQ ID NO:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                  LIBRARY: MYOMNOT01
CLONE: 779308
                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-855-140-2
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                                                           Sequence 938, Application US/09016434
| Sequence 938, Application US/09016434
| Patent No. 6500938
| GENERAL INFORMATION:
| APPLICANT: Jeffrey J Seilhamer |
| TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING |
| TITLE OF INVENTION: DATHWAY GENE EXPRESSION |
| NUMBER OF SEQUENCES: 1490 |
| CORRESPONDENCE ADDRESS: 1490 |
| STREET: 3174 PORTER DRIVE |
| COUNTRY: USA
                                                                                                                                                                                                                                                    ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
CLASSIFICATION NUMBER: US/09/016,434
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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CLASSIFICATION:
ATTORNEY FAGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAN: (650) 845-4166
INFORMATION FOR SEQ ID NO: 938:
SEQUENCE CHARACTERISTICS:
CHARACTERISTICS:
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TYPE: nucleic acid
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314 ATGGTGACGGGCTTCCTCGGCTGCCTGGGGGCCATCAAGGAAAAACAAGTGCCTCCTCCTC 373
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                                                                                                                                                                                                                                              115 PhevalPheLysAspTrpIleArgAspGlnLeuAsnPhePheIleAsnAsnAsnValLys 134
                                                                                                                                                                                                                                                                                     173 ThrAspLeuAsnProSerArgGluArgCysGlyValProPheSerCysCysValArgAsp 192
                                                                                                                        95 PhepheSerValPheLeuGlyLeuIlePhePheLeuGluLeuAlaThrGlyIleLeuAla 114
                                                                                                                                                                                                                                                                                                                                                                             135 AlaTyr----ArgAspAspIleAspLeuGInAsnLeuIleAspPheAlaGlnGluTyr 152
                                                                                                                                                                                                                                                                                                                                                                                                                 153 TrpSerCysCysGlyAlaArgGlyProAsnAspTrpAsnLeuAsnIleTyrPheAsnCys 172
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75 SerValLeuGlyPheAlaGlyCysIleGlyAlaLeuArgGluAsnThrPheLeuLeuLys 94
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Search completed: November 21, 2003, 17:14:15 Job time : 70 secs

Title:

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BG478644 60252532
B1909709 601070671
B191395 602109182
B158251 602291828
B1557863 601236858
B1829529 601080360
BE615323 601280719
BF043338 BPE56022B
ACA3350 Mus muscu
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A COT 25-NORMALIZED Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
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                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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CDNA clone CSODC029YJ10 5-PRIME, mRNA sequence.
AL528502 GI:31066352
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-MODEL=frame+ p2n. model -DEV=xlh
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-DB=EST -1/USPTO spool/US09972970/runat_21112003_125335_27239/app_query.fasta_1.391
-DB=EST -0FWT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOFCL=0 -LOOFEXT=0
-UNITS=b1ts -GTART=1 -END=-1 -MATRIX=b10sum62 -TRANS=human40.cdi -LIST-45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-UNFNT=pct -NORM=ext -HEAPSIXE=500 -MINLEN=0 -MAXLEN=2000000000
-USRS=US09972970 @CGN 1 1 2810 @runat_21112003 125335_27239 -NCPU=6 -ICPU=3
-NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPEDCCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                      November 21, 2003, 15:29:18; Search time 2152 Seconds (without alignments) 2631.479 Million cell updates/sec
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           GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                    - nucleic search, using frame_plus_p2n model
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Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Arakawa, M., Nishi, K., Yosawa, H., Kondo, S., Yamanaka, I., Saito, T., Saito, T., Saito, T., Saito, T., Saito, T., Saito, R., Kadota, K., Matsuda, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Fleischmann, W., Gasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Bodunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Marchlonni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H.,
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Mus musculus adult male stomach cDNA, RIKEN full-length enriched library, clone:2210021G21 product:F-BOX PROTEIN FBX23 (FRAGMENT) homolog [Homo sapiens], full insert sequence.
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   CAGIGLGGCTACGACGTCCGGCTCAAACTGGAGCTGGAGCAGGAGGGCTTCATCCACACC 931
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Rodentia, Sciurognathi; Muridae, Murinae, Mus.
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High-efficiency full-length cDNA cloning
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99279253
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AK008761 1 GT:12843154
HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
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Mammalia; Eutheria;
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                                                                              On Feb 13, 2001 this sequence version replaced gi:12791995.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 ENRY cedex - France
BP 191 91006 ENRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3528.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.ggi?seg=CSD0C029DE0SQP1&cluster=3528.f. Contact :
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODC029DE0SQP1.
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//Clone Type="NEUROBLASTOMA COT 25-NORMALIZED"
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//Clone Tib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
//Clone Tib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization
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AL529630 Homo sapiens NEUROBLASTOWA COT 50-NORMALIZED Homo sapiens
CDNA clone CSODD005YB20 5-PRIME, mRNA sequence.
AL529630
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                                                                                                                                                Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,710 full-length cDNAs

Lo for 770 full-length cDNAs

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Rackawa, T., Arawa, K., Akahira, S., Fukunishi, Y., Furuno, M., Haracka, T., Maraka, T., Furuno, M., Haracka, T., Maraka, T., Maraka, M., Kabukawa, T., Kato, H., Kawai, J., Kojima, Y., Komo, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, Y., Okido, T., Owa, C., Sakai, K., Salio, H., Sakai, C., Sakai, K., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Toya, T., Yamamura, T., Yakhaahi, F., Tanaka, T., Yoshino, M., Muramatuw, M. and Hayashizaki, Y., Toya, T., Yamamura, T., Yashino, M., Muramatuw, M. and Hayashizaki, Y., Dirett, Submission
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IPFLELAAGILAFVFKDWIRDQLNLFINNNVKAYRDDLDLQNLIDFAQEYWSCCGARG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (10-UIL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Fsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-rese@gc.riken.go.jp, URL.http://genome.gsc.riken.go.jp/, Tel:81-45-503-922, Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
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/note="unnamed protein product; F-BOX PROTEIN FBX23
(FRAGMENT) homolog [Homo sapiens] (SPTR|Q9UKB9, evidence: FASTY, 86.9%ID, 99.1%length, match=363)
putative"
Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.
Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001)
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Contact: Genoscope
Genoscope - Centre National de Sequencage
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Was normalized Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
3528 f For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi.bin/Cluster.cgi?Req=CSODD005DA10QP1xcluster=3528.f. Contact:
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODD005DA10QP1.
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/clone_Tist strand_coNA_was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA_was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCWNSPORT 6 vector. Library was normalized."
331 c 336 g 253 t 37 others
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                                                          Eukaryota; Metazoa; Chordata; Craniata; Verte
Mammalia; Eutheria; Primates; Catarrhini; Hon
1 (bases 1 to 1194)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
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BY708665 BIKEN full-length enriched, adult male stomach Mus mussulus cDNA clone 2210021G21 5', mRNA sequence.
                                                                             oSerValAlaMetMetSerGlySerAsnTrpSerTrpSerSerArgAlaProTyrThrPr 219
                                                                                                                                                                                                         Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute Fhe Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
ATTCGAGACCAGCTCAACCTCTTCATCAACAACGACGTCAAGGCCTACCGGGACGACATT 581
                                                                                                                                   181 ArgCysGlyValProPheSerCysCysValArgAspProAla----MetSerSerThrPr
                                                                                                                                                    CGCTGCGGGGTGCCCTTCTCCTGCTGCGTCAGGGACCCTGCGGAGGATGTCCTCAACACC
                                         S82 AACCTCCAGAACCTCATTGACTTTGCTCAGGAATACTGGTCTTGCTGCGGAGC-CGAGGC
                        oLysAlaValTrpAlaSerLeuArgSerGlyCysArgThrThr 233
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601279927F1 NIH_MGC_39 Homo sapiens CDNA clone IMACE:3621871 5', BE615772
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llh.gov

Plate: LLCM296 row: e column: 08

High quality sequence stop: 699.
81 GlyCyslleGlyAlaLeuArgGluAsnThrPheLeuLeuLysPhePheSerValPheLeu 100
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 849)

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                                                                                                                                                61 LeuAspProValTrpLeuPheValValValGlyGlyValMetSerValLeuGlyPheAla
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratcry in Riken Genomic Sciences Center and Genome Science Laboratcry in RIKEN. Division of Experimental Animal Research in Riken contributed to Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
            Email: genome-res@gsc.riken.go.jp,
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda
,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F., Imotani,K.,
,S., Hashizume,W., Kagawa,I., Kawai,J., Kojima,Y., Kondo,S., Kondo
,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K.,
Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N., Sano,H.,
Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Takeda,Y.,
Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="stomach"
/dev_stage="adult"
/lab_host="SOLR"
/clone_lib="RIKEN full-length enriched, adult male
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/db_xref="taxon:10090"
/clone="2210021G21"
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/organism="Homo sapiens"

/mol_type="mRNA"

/mol_type="mRNA"

/db_txefe="Laxon:9606"

/clone="IMAGE:664676"

/tissue_type="adenocarcinoma, cell line"

/tiss
                                                                                                     16-OCT-2002
                                                                                                                                                                                                                                                                                                                                                NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ArCc
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2885 row: j column: 16
High quality sequence stop: 649.
                                                                                                                                                                                                                                                                              Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AGENCOURT 10475185 NIH MGC_107 Homo варјенв cDNA clone
IMAGE:646576 5', mRNA веquence.
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/mol type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:362187"

/tissue_type="adenocarcinoma"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NH MGC 39"

/clone_lib="NH MGC 39"

/note="Organ: pancreas; Vector: pOTB7; Site_1: Xho1;

Site_2: EcoR1; cDNA made by oligo-dT priming.

Directionally cloned into EcoR1(Xho1 sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin

(University of California, Berkeley) using ZAP-cDNA synthesis kt (Stratagene) and Superscript II RT (Life
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|AGTGTGGCTACGACGTCAAACTGGAGCTGGAGCAGCAGCGCTTCATCCACAAA
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Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 901)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Kristi A. Egland, Ira Pastan

CDNA Library Preparation: Invitrogen Corp

CDNA Library Preparation: Invitrogen Corp

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Plate: LLAM1285 row: f column: 03

High quality sequence stop: 683.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bp mRNA linear EST 12-NOV-2002
) sapiens cDNA clone IMAGE:6722499 5',
                                                                                GlyLeullePhePheLeuGluLeuAlaThrGlylleLeuAlaPheValPheLysAspTrp 120
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                                                                                                                                                                                                                                                                                      652
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                                                                                                                                         121 IleArgAspGlnLeuAsnPhePheIleAsnAsnAsnValLysAlaTyrArgAspAspIle 140
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CTIGACCCCGIGIGGCIGITIGIGGIAGIIGGAGGCGICAIGICGGIGCIGGGCTIIGCI 352
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Subtracted with brain, liver, lung, kidney and muscle.
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                                                                                                                                                                                                                  GACCTCCAGAACCTCATTGACTTTGCTCAGGAATACTGGTCTTGCTGCGGAGCCCGAGGC
                                                                                                                                                                                                                                                                          CCAATGACTGGAACCTCAATATCTACTTCAACTGCACTGACTTGAACCCCAGCCGGGAG
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/organisma"Homo sapiens"
/mol type="mRNA"
/db_xref="taxon,9606"
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AGENCOURT 10735735 MAPCL HOMO
MRNA sequence
CA454987
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SOURCE
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TITLE
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Directionally cloned. Priming method: oligo-dT. Average insert size: 1800 bp. Library amplification: 26,000 fold. Kristi A. Egland. James J. Vincent, Robert Strausberg, Bungkook Lee & Ira Pastan: Discovery of new breast cancer genes encoding membrane and secreted proteins.

275 c 269 g 200 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 602719148F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:4839779 5', BG770931
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2 206
11
3 3
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                1.35e-95
1090.50
93.69%
92.79%
85.00%
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/clone="IMAGE:5441687"
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NOTE: The stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the stratage of the strata
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BM563474 GI:18810427
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                                                                                                                                                                                                                                                               AspLeuGlnAsnLeuIleAspPheAlaGlnGluTyrTrpSerCysCysGlyAlaArgGly 160
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                                                                                                                                                                                                                                                                                                                                                                                              609 CCCAATGAACCTCGAATATCTACTTCAACTGCACTGACTTGAACCCCAGCCGGGG 668
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NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ArG.
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboration
CDNA Library Preparation: Rubin Laboration
CDNA Library Argued by: The I.M. A.G.B. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M. A.G.B. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1916 row: f column: 24
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                   GlyLeuIlePhePheLeuGluLeuAlaThrGlyIleLeuAlaPheValPheLysAspTrp
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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Location/Qualifiers
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Homo sapiens
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                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (Dases 1 to 781)

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGL Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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                                                                                                                                                                                                                                                                             Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLCM1669 row: o column: 12
High quality sequence stop: 697.
Location/Qualifiers
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  BG770931.1 GI:14081584
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94.88%
94.42%
84.76%
                                                   Homo sapiens (human)
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239 c
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Best Local Similarity:
Query Match:
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VERSION
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JOURNAL
COMMENT
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/mol_type="makA"
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/clone="CS0D100SYMO""
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/clone=Tissue type="placenta"
/clone=Tissue the mapping primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCWVSPORT 6 vector. Library was normalized."
// a 279 c 288 g 205 t 9 others
Unpublished
On Feb 15, 2001 this sequence version replaced gi:12876393.
Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
Invitable Sequence Cope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3528.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi.bin/cluster.cgi?seq=CSODIO05AG04QP1&cluster=3528.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODIOO5AG04QP1.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished
Contact: Robert Strausberg, Ph.D.
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Tissue Procurement: ArCC/DCTD/DTP
CDNA Library Preparation: Ling Mang/Rubin Laboratory
CDNA Library Preparation: Ling Mang/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1404 row: K column: 06
High quality sequence stop: 734.
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Contact: Genoscope - Centre National de Sequencage
BP 191 91006 ENRY cedex - France
Email: seqrefégenoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Initrogen. This sequence belongs to sequence cluster 3528.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=cSODK005CD11QP1&cluster=3528.f. Contact:
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invirogen.com/ InvirroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODK005CD11QP1.
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1. (bases 1 to 1201)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization
Unpublished

On Feb 15, 2001 this sequence version replaced gi:12899797.
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/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
                                                         180 luArgCysGlyValProPheSerCysCysValArgAspProAla----MetSerSerThr
                                                                                                676 AGCGCTGCGGGGGTGCCCTTCTCCTGCTGCGGCGACGACCCTGCGGAGGATGTCCTCAACA
                                                                                                                                                                  199 ProSerValAlaMetMetSerGlySerAsnTrpSerTrpSerSerArgAlaProTyrThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Fmail: cgapbs-r@mail.nih.gov
Tissue Profurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM11621 row: j column: 01
High quality sequence stop: 712.
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602525532F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4643959 5', mRNA sequence.
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Contact: Sandy Clifton, Ph.D.
WashU Xenopus EST project, 1999
WashU Xenopus EST project, 1999
WashUngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
Library constructed by M. Kirschner (Harvard Medical School). DNA
Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.B. Consortium/LLNL at: info@image.llnl.gov
High quality sequence stop:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                          de61f11.y1 Kirschner embryo St10 14 Xenopus laevis CDN 24-JAN-2001 MAGE:3516428 5' similar to TR:060628 060628 TETRASPANIN TSPAN-5. EG017161 GI:12471136
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;

Xenopodinae; Xenopus.

(bases 1 to 714)

Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Pape, D., Martin, J., Wylie, T., Underwood, K., Theising, B., Bowers, Y., Person, M. Gibbons, M., Harvey, M., Ritter, E., Jackson, Y., McCann, R., Waterston, R. and Wilson, R.,

Watchi, L., L., L., Blumberg, B., Jackson, Y., McCann, R.,

Watch Xenopus EST project, 1999
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                                                                                                           GlyLeuIlePhePheLeuGluLeuAlaThrGlyIleLeuAlaPheValPheLysAspTrp 120
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/mol_type="mRNA"

/db_xref="traxon:9606"

/clone="MAGE:4643959"

/tissue_type="melanotic melanoma"

/tab host="DH10B (phage-resistant)"

/clone=lbH10B (phage-resistant)"

/clone=lbH10B (phage-resistant)"

/clone=lorgan: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoR1; cDNA made by oligo-dT priming. Directionally cloned into EcoR1/KhoI sites using the following 5' adaptor: GGCACGG(G). Size-selected 550bp for average insert size 1: 8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synchesis kit

(Stratagene) and Superscript II RT (Life Technologies)."
                                           S NIH-WGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC/DTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL)
http://image.llnl.gov
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Search completed: November 21, 2003, 17:13:02 Job time : 2160 secs

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gene therapy; autoimmune haemolytic anaemia; autoimmune thyroidtis; diabetes mellitus; alleray; Crohn's disease; multiple sclerosis; rheumatoid arthritis; ulcerative collitis; cardiovascular disorder; anyocardial ischaemia; neurological disease; antifungal; antiviral; antibacterial; cerebral anoxia; epilepsy; infectious disease;
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Copyright (c) 1993 - 2003 Compugen Ltd.
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	score	Match	Length	DB	ID	
_	1283	100	25.1B	24	AADOLGGA	
+ 7		94.7	2091	5 7	AAA96482	encoding a
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4.		94.5	1126	22	AAC90014	
Λ 4	1176 5	6. E. E.	1644	2.4	ABL90838 AB211816	Human polynucleot
۰,	958.5	74.7	1655	21	AAC98195	Human colon cancer
∞	955.5	74.5	1567	23	ACC44092	amma-hy
ο ;	918.5	71.6	1174	22	AAC90015	Clone HE8EJ16 cod
10	25.5	9.69	1178	2 5	AAC90020	Clone HEBEL16 cod
12	80.7	6.0	1110	2 0	A4220854 AA659291	Polynucieotide seq
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14	790	61.6	864	24	AAI72287	NET-4 antisense mo
15	759.5	59.2	1988	24	ABK35735	CDNA sequence #12
1 1	654.5	0.13	813	22	AAF90629	Human TANGO 339 C
1 5	654.0	21.0	2465	4 6	AAU29623 ARX70953	Novel buren cons
16	654.5	51.0	2715	2 2	AAF90628	Human TANGO 339 CD
50	653.5	50.9	813	22	AAF90656	Human TANGO 339 K
21	651.5	50.8	813	22	AAF90657	띭
2 6	651.5	9.00	2623	2 6	AAS92016 88590658	DNA encoding nove
24.	650.5	50.7	813	22	AAF90659	Human TANGO 339 H
25	641.5	50.0	2672	21	AAZ65259	Human secreted pr
56	635.5	49.5	1428	21	AAA93623	Human tetraspanin
27	583.5	45.5	1667	2 5	AA265350	₩.
5 6	537	41.9	368	2 5	AA293364	Semience encoding
30	537	41.9	368	24	AAL41055	CDNA of Human F-bo
31	490.5	38.2	839	22	AAH34927	Human colon cancer
3.5	482.5	37.6	810	23	ABL14835	Drosophila melano
. K	476.5	7.7.	1932	7 5	AA344005	Human correted ny
32	476.5	37.1	1932	5 2	AAD11660	Human secreted pro
36	476.5	37.1	1932	24	ABK69756	Human secreted pr
37	476.5	37.1	2384	24	ABZ11836	Human polynucleot
38	461.5	36.0	2638	4.	ABL90058	Human polynucleoti
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4 4	430	33.1	3009	23	ABL:14834	Hydrophobic domain Drocophila melanod
42	427.5	33.3	816	21	AAA93675	808
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					ALIGNMENTS	
RESULT 1						
B T Z	883	standard;	; cDNA;	253	8 BP.	
AC AAD	AAD21883;					
12	-FEB-2002	(first	st entry)	₹		
XX DE Human	an TM4SF	receptor	or-encoding	odino	gene 1 cDNA clone	HOFOB55, SEO ID NO:2.

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121 IleArgAspGlnLeuAsnPhePheIleAsnAsnAsnValLysAlaTyrArgAspAspIle 140
                                                                                                                                                                                                                                                                                                      AspLeuGlnAsnLeulleAspPheAlaGlnGluTyrTrpSerCysCyyGlyAlaArgGly 160
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                                                      CTCGACCCTGTGTGGCTGTTTGTAGTGGTTGGAGGCGTCATGTCCGTGCTGGGCTTTGCC 358
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                                                                                                             419 GGCCTCATCTTCTTCCTGGAGCTGGCAACAGGGATCTTGGCCTTCGTATTCAAGGACTGG
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                  LeuAspProValTrpLeuPheValValValGlyGlyValMetSerValLeuGlyPheAla
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Azimzai Y,
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16-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention tenders to numear attractions. Superstaning, trivention tenders to the invention of are useful for preventing, treating, ameliorating or diagnosing a pathological condition or a susceptibility to a pathological condition. The pathological condition or a susceptibility to a pathological condition. The pathological condition or pathological condition. The pathological condition or their activity. This mucleic acids, protein, antibodies, agonists and antagonists are useful in the diagnosis, treatment and prevention of cancer, particularly breast and ovarian cancer, and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenical; immune disorders such as Addison's disease, alabetes mellitus, crohn's disease, multiple sclerosis, theumatcid arthritis and ulcerative colitis; cardiovascular disorders such as cerebral anoxia and epilepsy; and infectious diseases such as cerebral anoxia and epilepsy; The present sequence is human TM4SF polymucleotides are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         238
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                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor polypeptides, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases
                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated protein, a member of 4-transmembrane superfamily of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to human 4-transmembrane superfamily (TM4SF)
                                                                                                          /*tag= a
/product= "Human TM4SF receptor protein"
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receptor protein encoding cDNA.
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 cancer;
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Best Local Similarity:
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antiparasitic;
                                                                                                                                                            WO200177173-A1
                                     Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence encodes a human transmembrane proteins (HTMP). Agonists and antagonists of the protein are used to treat a disease or condition associated with overexpression of the protein. Diseases and conditions which can be treated include cell proliferative, immunological, reproductive, smooth muscle and neurological disorders e.g. arteriosclerosis, myeloma, leukaemia, acquired immunodeficiency syndrome (AIDS), allergies, ovulatory defects, angina, hypertension, stroke, Alzheimer's disease, epilepsy and Tourette's disorder. The polynucleotides may be used to detect and quantify gene expression in biopsied tissues where protein expression may be correlated with disease e.g. to determine absence, presence or excess expression of HTMP or to monitor regulation of HTMP expression during therapeutic intervention.
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                                       New human transmembrane proteins are used to treat a disease or condition associated with decreased expression of functional HTMP e.g. Tourette's disorder, angina and leukaemia -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TrpAlaTrpGlyGluLysGlyValLeuSerAsnIleSerAlaLeuThrAspLeuGlyGly
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This sequence encodes tetraspanin 23228. This protein is a cell surface protein having four transmembrane domains (TM1-TM4). TM1, TM3 and TM4 have brotein having four transmembrane domains (TM1-TM4). TM1, TM3 and TM4 have brotein the a single polar anino acid located within them, which may interact with each other and contribute to domain stability. The cytoplasmic N-terminal domains and the intracellular loop between TM2 and TM3 and TM4 contains conserved Cys residues and may function between TM3 and TM4 contains conserved Cys residues and may function to bind extracellular growth factors, such as HB-EGF, TGF-alpha and campiregulin. The 23228 protein is useful for diagnosing and treating 1328 mediated disorders, e.g., haematopoletic and/or immune disorders such as diabetes mellitus, arthritis, multiple sclerosis, such as diabetes mellitus, crohr's diseases and asthma; cell proliferation and differentiation disorders, e.g., cancers or metastasis; and/or viral infections. 23228 polypeptide can control cellular signalling activity, bind to an extracellular growth factor, for example, amphiregulin, regulate cell proliferation, bind to a cell surface protein, to recruit intracellular kinases, to regulate cell contility, bind to another tetraspanin such as CD81, to associate with a
oSerValAlaMetMetSerGlySerAsnTrpSerTrpSerSerArgAlaProTyrThrPr 219
                   Gene; tetraspanin; 23228; cell surface protein; transmembrane domain; extracellular growth factor; HB-EGF; TGF-alpha; amphiregulin; diabetes mellitus; arthritis; multiple sclerosis; encephalomyelitis; dermatitis; Crohn's disease; and asthma; cancer; metastasis; viral infection; cellular signalling activity; cell proliferation; cell motility; CD81; B-Cell antigen receptor; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New tetraspanin 23228 polypeptide useful in screening assays, predictive medicine and as a prophylactic or therapeutic agent, e.g., for hematopoietic and immune diseases such as diabetes or multiple
                                                                              OLysAlaValTrpAlaSerLeuArgSerGlyCysArgThrThr 233
                                                                                                                         AAAGGCTGCGTGGCCAGTTTGAGAAGTGGCTGCAGGACAACC
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B-Cell antigen receptor and the ability to modulate the with a virus.
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                        676 A; 883
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Gene therapy; human; 4 transmembrane superfamily receptor protein; endocrine; cardiovascular; cerebrovascular disease; neural disorder; reproductive; skin; renal system; autoimmune; hyperproliferative; ocular; bacterial infection; viral; fungal; ss.
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03-JUN-1999; 99US-0137797.
11-JUN-1999; 99US-018573.
18-AUG-1999; 99US-0149447.
28-JAN-2000; 2000US-0178770.
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The invention relates to novel genes (ABL89449-ABL90853) and proteins (ABB896404) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, proteins, antibodies and (ant) agonists are useful in the diagnosis, proteins, antibodies and (ant) agonists are useful in the diagnosis, proteins, and orber of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, (c) immultiple solarosis, rheumarcid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) infectious diseases such as viral, bacterial, fungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LeuAspProValTrpLeuPheValValValGlyGlyValMetSerValLeuGlyPheAla
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                                                                                                                                                                                                                                                                                          Sequence 1644 BP; 297 A; 479 C; 513 G; 346 T; 9 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human polynucleotide SEQ ID NO 1400
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Length:
Matches:
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Mismatches:

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40

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160

701 180 761 199 821

Conservative: Mismatches: Indels:

Length: Matches:

.04e-104 1176.50 95.38* 95.38* 91.70

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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated polynucleotide (I) comprising a nucleotide sequence selected from any of 948 sequences (ABZ11119-ABZ12066) or their mature protein codding portion, active domain coding protein or complementary sequences. The polynucleotides are useful coding protein or complementary sequences. The polynucleotides are useful coding protein or complementary sequences. The polynucleotides are useful coding protein as a food supplement, for generating of human genome. The encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight markers, as a food supplement, for generating antibodies, in cell-proliferative disorders (cancer), neurodegenerative diseases (multiple cell-proliferative disorders (alecates), autoimmune diseases (multiple disorders, platelet or coagulation disorders, wound, burns, incision, ulcars, liver or lung fibrosis, infections (bacterial, viral, fungal, culcars, liver or lung fibrosis, infections (bacterial, viral, fungal, Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO.
                                                                                                                                                                                                                                                     Human; genome mapping; gene therapy; food supplement; virus; fungus; cell-proliferative disorder; neurodegenerative disease; bacterial; barkinson's disease; autoimmune disease; multiple sclerosis; diabetes; genetic disorder; wound; burn; infection; arthritis; cytostatic; immunoadulator; nootropic; neuroprotective; antiparkinsonian; antidiabetic; immunosuppressive; dermatological; haemostatic; vulnerary; fungicide; antibacterial; virucide; protozoacide;
                 881
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               CAGTGTGGCTACGACGTCCGGCTCAAACTGGAGCTGGAGCAGCAGCAGGGCTTCATCCACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotides comprising sequences assembled from expressed agequence tags (ESTS), useful for treating cell-proliferative, neurodegenerative, autonimmune, genetic, myeloid or lymphoid, or platelet or coagulation disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhao QA, F
Ghosh M;
Claim 1; SEQ ID NO 698; 1012pp + Sequence Listing; English
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l, Wang Z,
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                                         OLYBALAVAlTrpAlaSerLeuArgSerGlyCysArgThrThr
                                                              AAAGGCTGCGTGGCCAGTTTGAGAAGTGGCTGCAGGACAACC
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Yamazaki V, Chen R,
| D, Drmanac RT;
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Wang D,
                                                                                                                                    standard; cDNA; 1023
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P-PSDB; ABP69599.
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Alignment Scores:

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271 TGGGCTGCAATTGGGGCCCTCCGGGAGAACACCTTCCTGCTCAAGTTTTTCTCCGTGTTC 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; colon cancer; colon cancer antigen; diagnosis; detection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  218 rProLysAlaValTrpAlaSerLeuArgSerGlyCysArgThrThr 233
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690 160 750 180

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ArgCysGlyValProPheSerCysCysValArgAspProAla----MetSerSerThrPr 199
                                                                                                                                                                                                                                                                                                                                                                     gene; rat; gamma-hydroxybutyrate; anti-epileptic; anxiolytic; ds; antineurodegeneration; antipsychotic; brain; dopamine; opioid; GABA; gamma-aminobutyric acid; diagnosis; epilepsy; anxiety; sleep disorder; behavioral disorder; neurodegeneration; Parkinson's disease; psychosis;
                                                                                                                                                                                                                                   oSerValAlaMetMetSerGlySerAsnTrpSerTrpSerSerArgAlaProTyrThrPr
                    GlyLeuIlePhePheLeuGluLeuAlaThrGlyIleLeuAlaPheValPheLysAspTrp
                                       IleArgAspGlnLeuAsnPhePheIleAsnAsnAsnValLysAlaTyrArgAspAspIle
                                                                                                         |||:::|||||||||
| ATCAAAGACCAGCTGTATTTCTTTATAAACAACAACATCAGAGCATATCGGGATGACATT
                                                                                                                                                AspLeuGlnAsnLeulleAspPheAlaGlnGluTyrTrpSerCysCysGlyAlaArgGly
                                                                                                                                                                        ProAsnAspTrpAsnLeuAsnIleTyrPheAsnCysThrAspLeuAsnProSerArgGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New rat brain gamma-hydroxybutyrate receptor and its encoding nucleic acid, useful for identifying agents for treating e.g. epilepsy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents the cDNA sequence encoding a novel rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= a
/product= "gamma-hydroxybutyrate receptor"
                                                                                                                                                                                                                                                                                                                                                                                                              Rat gamma-hydroxybutyrate receptor cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP
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                                                                                                                                                                                                                                                                                                                                                                                                   AAC97991 to AAC98763 encode the human colon cancer associated proteins, called human colon cancer antigens, given in AAB51234 to AAB54006. The human colon cancer antigens can have cytostafic, cardioactive, muscular; neuroprotective, immunomodulatory, gynaecological, gastrointestinal, colon be used in gene therapy. The colon cancer antigen polymuclectides, and cancer in gene proteins and antibodies to the proteins are useful for the prevention, treatment and diagnosis of colon disorders, such as colon cancer. The polymuclectides may be used in diagnostics and research, such as for chromosome identification, and as hybridisation probes. The proteins may also be used to prevent disorders, such as neural disorders, immune system disorders, muscular disorders, reproductive disorders, immune diseases, and cardiovascular disorders. The diseases, and cardiovascular disorders. AAC99764 to AAC98772 and AAC987007 represent sequences used in the exemplification of the present
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                                                                                                                                                                                                                                                                                                           Colon cancer associated gene sequences, referred to as colon cancer antigens, useful for the treatment, prevention, and diagnosis of colon disorders such as colon cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Met ProGlyLygHisGlnHisPheGlnGluProGluValGlyCysCysGlyLysTyrPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 LeuPheGlyPheAsnIleValPheTrpValLeuGlyAlaLeuPheLeuAlaIleGlyLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LeuAspProValTrpLeuPheValValValGlyGlyValMetSerValLeuGlyPheAla
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Matches:
Conservative:
Mismatches:
infectious disease; cardiovascular disorder; ss.
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                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                               99US-0124270.
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958.50
84.19%
76.92%
                                                                                                                               08-MAR-2000; 2000WO-US05883
                                                                                                                                                                                                                             Ruben SM;
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Best Local Similarity:
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                                                                WO200055351-A1
                                                                                                                                                               12-MAR-1999;
                                Homo sapiens
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cell cDNA library. The invention relates to the isolation of this novel cell cDNA library. The invention relates to the isolation of this novel cell cDNA library. The invention relates to the isolation of this novel cell cDNA library. The invention relates to the sequence except for those homologues that having GenBank accession numbers AAC 17120 (human context of the man distance and is involved in regularing dopaminergic, opioid and GABA(gamma-aminobutyric acid) ergic activities. The nucleic acid that encodes the protein is used: (1) as primers or probes for detection/amplification, particularly for screening gene context of interactions and regulators of the GHBR gene; (2) for expression of recombinant polypeptides; and (3) to detect allelic abnormalities in the GHBR gene (for diagnosing diseases, or susceptibility, associated with abnormal expression of GHBR). The corrent for agents that interact with GHBR; (2) to study corrent for agents that interact with GHBR; (2) to study corrent for agents that interact with GHBR; (2) to study corrent for agents that interact with GHBR; (2) to study corrent for agents that interact with GHBR; (2) to study corrent for agents that interact with GHBR; (2) to study corrent for agents that interact with GHBR; (2) to study corrent for agents that interact with GHBR; (2) to study corrent for agents or activity of GHBR, particularly those involving cerebral GABA(gamma-aminobuyts, and (3) to raise antibodies (Ab) specific for GHBR. The agents are used to prevent or treat diseases associated with abnormal correlation of activity of GHBR, particularly those involving cerebral correlation and regulation of section of hormones (growth hormone correction of hormones (growth hormone) and and regulation of section of hormones (growth hormone correction and and regulation of section of hormones (growth hormone).
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Sequence 1567 BP; 281 A; 436 C; 480 G; 370 T; 0 other;

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                                                                                                                            1 MetProGlyLysHisGlnHisPheGlnGluProGluValGlyCysCysGlyLysTyrPhe
                                                                                                                                                                                  LeuPheGlyPheAsnIleValPheTrpValLeuGlyAlaLeuPheLeuAlaIleGlyLeu
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                                                                                                                                                                                                                                                                                      YLeuAspProValTrpLeuPheValValValGjyGjyValMetSerValLeuGjyPheAl
                                                                                                                                                                                                                                                                                                        aGlyCys11eGlyAlaLeuArgGluAsnThrPheLeuLeuLysPhePheSerValPheLe
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            Length:
Matches:
Conservative:
Mismatches:
                                                                                                      US-09-972-970-4 (1-233) x ACC44092 (1-1567)
            5.22e-83
                       955.50
85.11%
82.13%
74.47%
                                      Percent Similarity:
Best Local Similarity:
Alignment Scores:
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Sequence 1174 BP; 306 A; 259 C; 291 G; 316 T; 2 other;

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GGluArgCy8GlyValProPheSerCy8Cy8ValArgA8pProAlaMetSerSerThrPr 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene therapy; human; 4 transmembrane superfamily receptor protein; addocrine; cardiovascular; cerebrovascular disease; neural disorder; reproductive; skin; renal system; autoimmune; hyperproliferative; ocular; bacterial infection; viral; fungal; ss.
                                                                                                                                   134 ACCCATGTGGCTATACATCCGCTCAAACTG-AGCTGGAGCACAAGATTCATCTACACCAA 792
615 GCCCAATGACTGGAACCTCCAACATCCGGACTTCAACTGCACTGACTTCAAACCCAAGCCG 674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to isolated nucleic acids and proteins encoding human soluble 4 transmembrane superfamily receptor protein (see Acc90102-200023) and AAB49502-B49513). The present sequence is one such nucleic acid. The present sequence is useful for preventing, treating or ameliorating a medical condition and in diagnosing (susceptibility to) a pathological condition e.g. endocrine disorders e.g. Addison's disease, (ardio)vascular diseases, neural disorders e.g. Alzheimer's and Parkinson's disease, reproductive disorders e.g. Alzheimer's and psoriasis, renal system disorders e.g. him disorders e.g. psoriasis, renal system disorders e.g. nephritis; (auto)immune system disorders e.g. set the pancreas, ocular disorders e.g. glaucoma and infections caused by bacteria, viruses and fungi.
                                                                CBACCCTGTGGGGTGCCCTTCTGCTGGTAAG-GACCCTGCGGAAGACGTCTCAAT
                                                                                                              199 oSerValAlaMetMetSerGlySerAsnTrpSerTrpSerSerArgAlaProTyrThrPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated nucleic acid molecule encoding human soluble 4 transmembrane superfamily receptor protein, useful for diagnosing, treating and/or preventing disorders e.g. Alzheimer's, cancer and arrhythmia -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ni J, Fan P, Roschke V, Shi Y, Komatsoulis GA;
                                                                                                                                                                                      219 oLysAlaValTrpAlaSerLeuArgSerGlyCysArg 231
                                                                                                                                                                                                                         793 AGCTGGT-----GGCCATTTGAGAAGTGGCTCAAGA 823
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03-UTM-1999; 99US-0137797.
11-UTM-1999; 99US-013673.
18-MUS-1999; 99US-0149447.
28-JAN-2000; 2000US-0178770.
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                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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Rosen CA;
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99US-0137797.
99US-0138573.
99US-0149447.
                                                                                                                        (HUMA-) HUMAN GENOME SCI INC
                                                                                                      28-JAN-2000; 2000US-0178770.
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892.50
82.70%
75.53%
69.56%
                                                   2000WO-US13504
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Best Local Similarity:
Query Match:
DB:
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                WO200070076-A1
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                                                                    19-MAY-1999;
03-JUN-1999;
11-JUN-1999;
Ното варіепв
                                                   18-MAY-2000;
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                                  23-NOV-2000
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                                                                                                                                         Ruben SM,
Rosen CA;
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                                                                                                                     LeuPheGlyPheAsnIleValPheTrpValLeuGlyAlaLeuPheLeuAlaIleGlyLeu
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83.40%
76.17%
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                                  Similarity:
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The present invention relates to isolated nucleic acids and proteins encoding human soluble 4 transmembrane superfamily receptor protein (see PAC90012-290023 and AAB4502-849513). The present sequence is one such nucleic acid. The present sequence is useful for preventing, treating or ameliorating a medical condition and in diagnosing (susceptibility to) apathological condition e.g. endocrine disorders e.g. Addison's disease, (cardio)vascular diseases, neural disorders e.g. Alzheimer's and Parkinson's disease, reproductive disorders e.g. Alzheimer's and Parkinson's disease, reproductive disorders e.g. Alzheimer's and Psoriasis, renal system disorders e.g. nephritis, (auco)immune system disorders e.g. not disease, hyperproliferative disorders e.g. necoplasms of the pancreas, coular disorders e.g. glaucoma and infections caused by bacteria, viruses and fungi.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated nucleic acid molecule encoding human soluble 4 transmembrane superfamily receptor protein, useful for diagnosing, treating and/or preventing disorders e.g. Alzheimer's, cancer and arrhythmia -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Met Progly Lys His Gluhis Phe Glu Glu Proglu Val Gly Cys Cys Gly Lys Tyr Phe
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AspLeuGlnAsnLeulleAspPheAlaGlnGluTyrTrpSerCysCysGlyAlaArgGly 160
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               CGGGAATTATTTTTTTTTCTGGAGCTCACTGCCGGAGTTCTAGCATTGTTTTCAAAGAC
                                         TrplleArgAspGlnLeuAsnPhePhelleAsnAsnAsnValLysAlaTyrArgAspAsp
                                                                         IleAspLeuGlnAsnLeuIleAspPheAlaGlnGluTyrTrpSerCysCysGlyAlaArg
                                                                                   GluArgCysGlyValProPheSerCysCysValArgAspProAla----MetSerSerTh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polynucleotides encoding human secreted proteins used for therapeutic, diagnostic and research purposes.
                                                                                                                                                                                                                rProLysAlaValTrpAlaSerLeuArgSerGlyCysArgThr 232
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                                                                                                                                                                                                                              744 ACGAAAGGCTGTGTGCCCCAGTTTGAGAAGTGGTTGCAGGACA
                                                                                                                                                                                                                                                                                                                                       secreted protein; cDNA library; clone; transmembrane signal sequence cloning; hybridization cloning; gene
                                                                                                                                                                                                                                                                                                                     Polynucleotide sequence of the dk329_1 clone.
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, Steininger
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Treacy M, Agostino MJ,
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P-PSDB; AAY42381.
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17-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                            receptor;
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This is the polynucleotide sequence of the clone dk129 1, which was isolated from a human fetal kidney cDNA library using methods which are selective for cDNAs encoding secreted proteins, or by identification as a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein (AAY42181).

The PNB and proteins of the invention are predicted to have biological activities which would make them sultable for treating preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, immune stimulating (e.g. as vaccines) or suppressing activity, hemostatic activity, chemotopiesis regulating activity, these growth activity, hemostatic activity, chemotocic/chemokinetic activity, and tumor inhibition activity, receptor/ligand activity, and tumor civity. The PNS are also stated to be useful for gene therapy. Other activities include inhibiting the growth, infection or bacteria, fungi, viruses and other parasites; effecting function of bacteria, fungi, viruses and other parasites; effecting blothythms or circadian cycles; enhancing fertility; treatment of pain; hormonal or endocrine activity.
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Claim 12; Page 101; 125pp; English.
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76.50%
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Best Local Similarity:
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The invention relates to novel human secreted proteins, the nucleic acids encoding them. The protein may exhibit cytokine, cell proliferation or cell differentiation activity or may induce production of other cytokines in certain cell populations and may exhibit immune stimulating or immune suppressing activity, which is useful for the treatment of various immune deficiency (SCID), which is useful for the treatment of immunodeficiency (SCID), autoimmune disorders e.g. severe combined immunodeficiency (SCID), autoimmune disorders e.g. multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation. The proteins are also useful in the treatment of diseases and disorders including tissue, skin and organ transplantation and in graft-versus-host diseases (GVHD), in the induction of tumour immunity,
  ArgCysGlyValProPheSerCysCysValArgAspProAla----MetSerSerThrPr 199
                         oSerValAlaMetMetSerGlySerAsnTrpSerTrpSerSerArgAlaProTyrThrPr 219
                                                                                                                 CAGTGTGGCTATGATGCCAGGCAAAAACCAGAAGTTGACCAGCAGATTGTAATCTACACG 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mumban, secrete plocetin; bas; autituitammacors; autimidate processive; nootropic; neuroprotective; autimithic autimicrobial; vulnerary; cytostatic; autidiabetic; virucide; autimifertility; auticonvulaant; vasotropic; autiparkinsonian; immunostimulant; dermatological; antitheumatic; antituon; antiulicer; osteopathic; tranquilser; cerebroprotective; cytokine; cell proliferation; cell differentiation; immune deficiency; severe combined immunodeficiency; SCID; tumour; autoimmune disorder; multiple sclerosis; rheumatoid arthritis; graft-versus-host disease; myeloid deficiency; wound healing, ulcer; periodontal disease; osteoporosis; osteoarthritis; Alzheimer's disease; stroke; sepsis; inflammatory bowel disease; contraceptive; immunogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Secreted human proteins, useful as vaccine for treating various diseases such as autoimmune disorders (e.g. multiple sclerosis), and nervous system disorders (e.g. stroke) -
                                                                                                                                                                                                                                                                                                                                                                                                                                         secreted protein; 88; antiinflammatory; immunosuppressive;
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Agostino MJ, Steininger RJ, Spaulding V,
Fechtel K, Merberg D;
                                                                                                                                                                                      OLYSAlaValTrpAlaSerLeuArgSerGlyCysArgThr 232
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                                                                                                                                                                                                                                                                              AASS9291 standard; cDNA; 1110
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04-DEC-2000; 2000US-0729674.
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Treacy M,
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            in the treatment of burns, incisions and ulcers; as well as in treatment of periodontal disease, osteoporosis or osteoarthritis, mediated by inflammatory processes, diseases of the peripheral nervous system, Alzheimer's, Parkinson's disease, Huntington's disease, amylotrophic lateral sclerosis, and Shy-Drager syndrome, infections, infarction of cardiac and central nervous system vessel e.g. stroke, sepsis, inflammatory bowel disease, ulcers, bone regeneration. The protein, having activin or inhibin-related activities is useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. The proteins and nucleic acids are also useful as food supplements. The proteins and nucleic acids are also useful as food supplements. The present sequence encodes a secreted protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141 AspLeuGlnAsnLeulleAspPheAlaGlnGluTyrTrpSerCysCysGlyAlaArgGly 160
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myeloid or lymphoid cell deficiencies, wound healing and tissue repair,
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Matches:
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Human; clone bd106-7; clone yb8-1; ATCC number 98599; gene therapy; immune disorder; bacterial infection; fungal infection; cancer; tumour; autoimmune disorder; systemic lugus erythematosus; wound; ulcer; inhibin; osteoporosis; osteoarthritis; nervous system disorder; neuropathy; Alzheimer's disease; Parkinson's disease; Huntington's disease; activin; haemophila; cardiac infarction; stroke; sepsis; archritis; vulnerary; ischaemia-reperfusion injury; inflammatory bowel disease; chemotactic; crohn's disease; chemotactic; neuroprotective; haemostatic; thrombolytic; anti-inflammatory; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to isolated polynucleotides (ABA90876-ABA90968 and ABA90980) and encoded proteins (ABB55698-ABB55800), especially polynucleotides SEQ ID NO 1 (ABA90876) and SEQ ID NO 19 (ABA90885) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New secreted proteins and encoding polynuclectides, useful in gene therapies, particularly for preventing or treating autoimmune disorders, cancer, graft-versus-host disease, wound, osteoporosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Collins-Racie LA, Evans C;
Steininger RJ, Spaulding
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                                                                                Human polynucleotide SEQ ID NO 169
           ВР
           ABA90960 standard; cDNA; 1110
                                                                                                                                                                                                                                                                                                                              97US-126425P.
97US-067454P.
97US-06743P.
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EVANS C.
MERBERG D.
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AGOSTINO M J.
STEININGER R J
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Clark H, F
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LAVALLIE E R.
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CLARK H.
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Wong GG,
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(MERB/)
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(STEI/)
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ABA90960
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processing Set 10 No. 2 (ABBSDS99) and Set 10 No. 2 (ABBSDS9707) contained in clones bd306-7 and yb8-1 respectively and the clones bd306-7 and yb8-1 are deposited with the American Type Culture Collection (ATCC) with accession number 98599. The polymucleotides and encoded polypeptides have cytostatic, anti-inflammatory immunomodulator, vulnerary.

Cytostatic, anti-inflammatory immunomodulator, themostatic, thrombolytic and anti-inflammatory activity and acting as cytokine modulators, thrombolytic and anti-inflammatory activity and acting as cytokine modulators.

Commandatopiesis regulators, tissue growth modulators and/or cadherin suppressors. The polypeptides and polymucleotides are useful in gene the following diseases: immune deficiency and disorders; e.g. bacterial cort fungal infections, autoimmune disorders, cancer, systemic lupus erythematosus or graft-versues host disease; myeloid or lymphoid cell deficiencies; wound, burns, incisions and ulcers, osteoporosis or certorathies, eog. Alzheimer's Parkinson's disease and neuropathies, eog. Alzheimer's Parkinson's disease, amyotrophic lateral sclerosis or Shy-Drager syndrome; cort systemic inflammatory response syndrome; systemic inflammatory response syndrome, is chosen, ereperfusion or stroke, inflammations, shock, sepsis or systemic inflammatory response syndrome; including vulgaris or pemphigus control.
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SEQ ID NO 2 (ABB55698) and SEQ ID NO 20 (ABB55707) contained
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LeuPheGlyPheAsnIleValPheTrpValLeuGlyAlaLeuPheLeuAlaIleGlyLeu

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61 LeuAspProValTrpLeuPheValValValGlyGlyValMetSerValLeuGlyPheAla

522 TTTGACCCAGTTTGGCTCTTCCTTGTGGTGGGAGGAGTGATGTTCATTTTGGGATTTGCA

462 TGGGCATGGAATGAAAAGGAGTTCTGTCCAACATCTTCCATCACCGCTGCGGC

TrpAlaTrpGlyGluLysGlyValLeuSerAsnIleSerAlaLeuThrAspLeuGlyGly

41

GlyCys1leGlyAlaLeuArgGluAsnThrPheLeuLeuLysPhePheSerValPheLeu 100

582 GGGIGCATIGGAGCGCIACGGAAAACACTITCCTTCTCAAGTITITITCGIGTICCTG

GlyLeuIlePhePheLeuGluLeuAlaThrGlyIleLeuAlaPheValPheLysAspTrp 120

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141 AspLeuGlnAsnLeulleAspPheAlaGlnGluTyrTrpSerCysCysGlyAlaArgGly 160

762 GATTTGCAAAACCTCATAGACTTCACCCAGGAATATTGGCAGTGCTGTGGGCTTTTGGA

BP

ABK35735 standard; cDNA; 1988

(first entry)

08-MAY-2002

ABK35735;

121 ileArgAspGlnLeuAsnPhePheIleAsnAsnAsnValLysAlaTyrArgAspAspIle 140

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CGATGTGGCGTTCCATTCTCCTGCTGCACTAAAGATCCCGCAGAAGATGTCATCAACACT 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents a NET-4 antisense molecule which acts as a NET-4 modulator. The modulator is useful for decreasing the expression of NET-4 in a mammalian cell, and for treating neoplastic disease, such that the neoplastic disease is reduced in severity. Modulators of NET-4 are also useful for regulating cell proliferation, and for controlling gene expression through triple helix formation which promotes the ability of the double helix to open sufficiently for the binding of polymerase, transcription factors or regulatory molecules. A NET-4 modulator is useful as drug for supplementing cancer therapeutics and other agents. It is also useful in other diseases of hyperproliferation, and to inhibit tumour cell
                                                     706 CAGTGTGGCTATGATGCCAGGCAAAAACCAGAAGTTGACCAGCAGATTGTAATCTACACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel NET-4 modulator useful for decreasing expression of NET-4 in a mammalian cell and treating neoplastic disease, is selected from antisense oligonucleotide, ribozyme, protein, polypeptide and a small
                                                                                                                                                                                                                                                                                NET-4; antisense; modulator; neoplastic disease; cell proliferation; gene expression; triple-helix; polymerase; transcription factor; cancer therapy; hyperproliferation; tumour; growth; invasion;
                                                                               other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162 A; 229 C; 249 G; 224 T; 0
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                                                                                                                                                                     ВР
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          growth, invasion or metastasis.
                                                                                                                                                                   standard; cDNA; 864
                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUN-2001; 2001WO-US18415.
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                                                                                                                                                                                                                                                                                                              cancer therapy, metastasis; ss
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Human secreted protein, hyperproliferative disorder, autoimmune disorder; immune deficiency disorder; blood disorder; inflammatory disorder; infectious disorder; allergic condition; neurodegenerative disorder; liver fibrosis; coagulation disorder; gene therapy; antimicrobial; tumour; cancer; hepatotropic; immunosuppressive; antirheumatic; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Six hundred and twenty three polynucleotides derived from a variety of human tissue sources which encode secreted proteins, useful for treating immune deficiencies and disorders such as autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                   Lavallie ER, Collins-Racie LA, Evans C;
Agostino MJ, Bowman MR, Spaulding V, Wong GG;
Howes SH, Resnick RJ, Gulukota K, Graham JR;
                                                                                          cDNA sequence #126 encoding novel human secreted protein.
                                                                                                                                                                                                                                                                                                                                     06-APR-2000; 2000US-195605P.
                                                                                                                                                                                                                                                                                                         29-MAR-2001; 2001WO-US10232.
                                                                                                                                                                                                                                                                                                                                                                      (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                   Merberg D, Treacy M,
Clark HF, Fechtel K,
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                                                                                                                                                                                                                                                                                                                                                                                                       McCoy JM,
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                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                                                                                                            18-OCT-2001.
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864 1139 129 1

Conservative: Mismatches: Indels: Gaps:

US-09-972-970-4 (1-233) x AAI72287 (1-864)

Length: Matches:

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790.00 88.51% 79.89% 61.57%

Similarity:

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The present invention relates to the isolation of novel cDNA sequences which encode human secreted proteins. The cDNA sequences have been derived from a variety of human tissues. The invention also provides a method for producing proteins from these polynucleotide sequences. The proteins are useful for identifying compounds that modulate their activity and production. The sequences of the invention are useful for identifying compounds that modulate their useful for treating disease such as hyperproliferative disorders (e.g. cancer), immune deficiency disorders (e.g. multiple classediciency (SCID)) autoimmune disorders (e.g. multiple classediciency (SCID)), autoimmune disorders (e.g. multiple classediciency (SCID)), infertious disorders (e.g. thepatitis), allergic conditions (e.g. athma), neurodesenerative disorders (e.g. hapatitis), allergic conditions (e.g. asthma), neurodesenerative disorders (e.g. hapatitis), haemophilia), and tumours. The polynucleotide sequences of the invention are also useful in gene therapy. ABK35510-ABK36232 represent the cDNA sequences of the invention that encode for novel human
                                                                                                                                                                                                                                                                                                                       Claim 1; Page 146; 393pp; English
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QQ	2 IC	TGGAATGAAAAGGAGTTCTGTCCAACATCTCTTCCATCACCGATCTCGGCGGCTTTGAC 61
ò	63 P1	lvalGlyGlyValMetSer
QQ	62 CC	CCAGTTTGGCTCTTCCTTGTGGGGAGGAGGAGGATCATTTGGGATTTGCAGGGGGC 121
ò	83 II	lleGlyAlaLeuArgGluAsnThrPheLeuLeuLysPhePheSerValPheLeuGlyLeu 102
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ò	103 IJ	llePhePheLeuGluLeuAlaThrGlylleLeuAlaPheValPheLysAspTrplleArg 122
qq	182 AT	ATTICITICTICCTGGAGCTCACTGCCGGAGTTCTAGCATTTGTTTTTCAAAGACTGGATCAAA 241
'n	123 AE	AspGlnLeuAsnPhePheIleAsnAsnAsnValLysAlaTyrArgAspAsplleAspLeu 142
QQ	242 GP	GACCAGCTGTATTTCTTTATAAACAACAACAACAGGAGGCTATCGGGATGACATTGG 301
8	143 GJ	GlnAsnLeulleAspPheAlaGlnGluTyrTrpSerCysGyAlaArgGlyProAsn 162
qq	302 CA	CAAAACCTCATAGACTTCACCCAGGAATATTGGCAGTGCTGTGGGGGCTTTTGGAGCTGAT 361
ò	163 As	AspTrpAsnLeuAsnleTyrPheAsnCysThrAspLeuAsnProSerArgGluArgCys 182
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Search completed: November 21, 2003, 15:34:34 Job time : 285 secs

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-DB=GenEmb1 -QEWT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
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-USER=USO9972970 @CGN 1 1 3508 @runat 21112003 125335 27229 -NCPU=6 -ICPU=3
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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AX42vaco ESCO10346 Mus muscu AF065389 Homo sapi
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AC061778 Sequence
BC041304 Xenopus 1
AF121344 Mus muscu
AF053455 Homo sapi
AC024427 Homo sapi
BD135990 Secretory
AX341015 Sequence
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AF311903 Homo sapi
AL116638 Homo sapi
AL116638 Homo sapi
AC10220 Homo sapi
AC175142 Rattus no
AC13095 Rattus no
AC13095 Rattus no
AC13095 Rattus no
AC13095 Rattus no
AC13095 Rattus no
AC13095 Mus muscu
AX47836 Sequence
BC04424 Homo sapi
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AC01737 Drosophil
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BC010405 Homo sapi
AX420466 Sequence
                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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ALIGNMENTS

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Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (basea 1 to 2426)

Strausberg, R.L., Feingold, B.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Schemen, C.M., Schuler, G.D., Altschul, S.P., Zeeberg, B., Buetow, K.H., Schaefer, C.K., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S. Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunatane, P.H., Richards, S., Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Vilalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Butterfield, Y.S., Krzywinski, M.J., Skalska, U., Snailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.B., Good full-length human and mouse chan lixital analysis of more than 15,000 full-length
                                                                                                                                                                              LUN-2003

Homo sapiens hypothetical protein MGC14859, mRNA (cDNA clone MGC:14859 IMAGE:3621871), complete cds.

BC010405

BC010405.1 GI:14714540
                                      601 cagricrescraceacercescreaacresascresascresascascascerrearceacace 660
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Submitted (09-JUL-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbe-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
bnk Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@aystemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
    OSerValAlaMetMetSerGlySerAsnTrpSerTrpSerSerArgAlaProTyrThrPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
                                                                           /organism="Homo sapiens"
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Strausberg, R.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: WO 0216603-A 3 28-FEB-2002;
Millennium Pharmaceuticals, Inc. (US)
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233 c 235 g 196
                  AX420468 813 bp
Sequence 3 from Patent W00216603.
AX420468
AX420468.1 GI:21524616
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1215.50
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Leiby, K.R.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
     601 GGCTGCGGGGTGCCCTTCTCCTGCTGCGTCAGGGACCCTGCGGGAGGATGTCCTCAACACC
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23228, a human tetraspanin family member and uses thereof
Patent: WO 0216603-A 1 28-FEB-2002;
Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
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Conservative:
Mismatches:
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Sequence 1 from Patent WO0216603.
AX420466
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96.60%
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Query Match:
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AUTHORS
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Mismatches:
Indels:
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 5 Row: f Column: 18.
Location/Qualifiers
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417 c 461 g 361 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="Mammary tumor. WAP-TGF alpha model. 7 months old, gross tissue."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 LeuAspProValTrpLeuPheValValValGlyGlyValMetSerValLeuGlyPheAla 80
          Email: cgapbs.romail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
DNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I M.A.G. E. Consortium (LLNL)
DNA Sequencing Center
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Gontact: ang@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, I Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 TrpAlaTrpGlyGluLysGlyValLeuSerAsnIleSerAlaLeuThrAspLeuGlyGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="RIKEN cDNA 2210021G21"
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136_.948
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Contact: MGC help desk
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1. (bases 1 to 1516)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetcw, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

McKernan, K.J., Malak, J.A., Qunaratne, P.H., McKand, F.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Generation and intial analysis of more than 15,000 full-length

MLD Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1516 bp mRNA linear ROD 16-APR-2003
Mus musculus RIKEN cDNA 2210021G21 gene, mRNA (cDNA clone MGC:6941
IMAGE:2811935), complete cds.
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Submitted (05-JUL-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                           GlyLeuIlePhePeLeuGluLeuAlaThrGlyIleLeuAlaPheValPheLysAspTrp
                                                                                                                                           NIH-MGC Project URL: http://mgc.nci.nih.gov
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GVLSNISSITDLGGFDPVWLFLVVGGWFILGFAGCIGALRENTFLLKFFSVFLGIIF
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MGCVPQPFEKKLQDNLITVAGIFALGIFGICLAQNLVSDIEAVRASW"
357 c 387 g 352 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chases 1 to 1405)
Rubinstein E., Serru, V. and Boucheix, C.
Direct Submission
Submitted (14-MAY-1998) INSERM U268, 14 av Paul Vaillant Couturier, Villejuif 94807, France
Location/Qualifiers
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                                                                               IleArgAspGlnLeuAsnPhePheIleAsnAsnAsnValLysAlaTyrArgAspAspIle 140
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AspLeuGlnAsnLeu1leAspPheAlaGlnGluTyrTrpSerCysCysGlyAlaArgGly
                                                                                                                                                               GlyLeuIlePhePheLeuGluLeuAlaThrGlyIleLeuAlaPheValPheLysAspTrp
                                                   ATCCGAGACCAACTTAATCTCTTCATCAACAATGTCAAAGCCTACCGGGATGATCTC
                                                                                                                                  ArgCysGlyValProPheSerCysCysValArgAspProAla----MetSerSerThrPr
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1405)
Serru,V., Dessen,P., Boucheix,C. and Rubinstein,E.
Sequence and expression of seven new tetraapans
Biochim. Biophys. Acta 1478 (1), 159-163 (2000)
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/codon seart=1

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/db_xref="GI:3152703"
                                                                                                                                                                                                                                                                                                                                                      AF065389 1405 bp
Homo sapiens tetraspan NET-4 mRNA,
AF065389
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Organism="Homo sapiens"

/mol_type="mRNA"

/db xref="taxon:9606"

/clone="IMAGE ID 219547"
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BCUUY704
HOMO Bapiens, tetraspan 5, clone MGC:9300 IMAGE:3895933, mRNA, complete cds.
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Strausberg,R.
                                                                                                                  41 TrpAlaTrpGlyGluLysGlyValLeuSerAsnIleSerAlaLeuThrAspLeuGlyGly
                                                                                                                                                                                                          MetProGlyLysHisGlnHisPheGlnGluProGluValGlyCysCysGlyLysTyrPhe
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 Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                           Gape:
                                                                              US-09-972-970-4 (1-233) x AF065389 (1-1405)
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2.6e-73
958.50
84.19%
76.92%
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Homo sapiens
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AUTHORS
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DQLNLFINNVKAYRDDIDLUNIDFAGFWSCARGPDDWNININIRFSTRTAFTSNPSR

BRCGVPFFCWVRTLMKFGOYFCGYTSAQTELEHKIHLHQSWWPFEKWLKKPDGWPGLA

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VCLCLCWRVRGWHYCALVGTPGGLNWGCTGAGLGHGFTTELCWCVCVCVCVCVCV

VCLCLCWRVRGWHYCALVGTPGGNPWGCHSLEWGPRILLWDV

SLCCLGGAGCCLRFLHHHDLEPAWSSPWPQCHSLEMGPRILLSVSLSRLPLRHTWQDGY
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
                                                                                                                                                    628 GGAATTATTTTCTTCCTGGAGCTCACTGCCGGAGTTCTAGCATTTGTTTTCAAAGACTGG
                                                                                                                                                                                                                                                             808 GCTGATGATGGAACCTAAATATTACTTCAATTGCAGAGTGCAAGAG
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     IleArgAspGlnLeuAsnPhePheIleAsnAsnAsnValLysAlaTyrArgAspAspIle
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                                                             568 GGGIGCATIGGAGCGCTACGGGAAAACACTTICCTICAAGTITITITICTGTGTICCTG
                                                                                                                    GlyLeuIlePheLeuGluLeuAlaThrGlyIleLeuAlaPheValPheLysAspTrp
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Organism="Rattus sp."

//nol_type="genomic DNA"

/db xref="taxon:10118"

22. 1560
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Sequence 2 from Patent WO0078948.
AX061778
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/ codon_start=1
/ codon_start=1
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/ product="tertaspan 5"
/ protein_id="AAH09704.1"
/ db_xref="G1:16307231"
/ db_xref
                                                                                                                                                          Contact: MGC help desk

Email: cgapbs-r@mail.nih.gov

Tissaue Procurement: ATC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome

Center, Stanford University School of Medicine, Stanford, CA 94305

Meb site: (Dickson, Mark) mcd@paxil.stanford.edu

Contact: (Dickson, Mark) mcd@paxil.stanford.edu

Bickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,

R. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             be found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortiun/LLML at: http://image.llnl.gov Series: IRAK Plate: 14 Row: h Column: 4
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21264582.

1. 1416
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Direct Submission
Submitted (29-JUN-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LeuPheGlyPheAsnIleValPheTrpValLeuGlyAlaLeuPheLeuAlaIleGlyLeu
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/loone Ilb="NIH MGC_70"
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Matches:
Conservative:
Mismatches:
Indels:
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Submitted (16-DEC-2002) National Institutes of Health, Xenopus Gene Collection (XGC), National Institute of Child Health and Human Development, 6100 Executive Boulevard, Room 4B01, Rockville, MD 20892-7510, USA
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                                                                                                                                                                                                                   Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 94 Row: g Column: 18
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MetProGlyLysHisGlnHisPheGlnGluProGluValGlyCysCysGlyLysTyrPhe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH-MGC Project
Contact: XGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Igor Dawid
Tissue Procurement: Dr. Igor Dawid
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradi
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                                                                                                                                                                                                                                                                                        /tissue type="Embryo, stage 31/32, Xenopus"
/clone Tib="NICHD_XGC_Emb4"
/lab_host="DH108"
/note="Vector: pCMV-SPORT6"
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175
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Matches:
Conservative:
Mismatches:
Indels:
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/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="IMAGE:4683897"
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74.40%
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Xenopus laevis, Similar to transmembrane 4 superfamily member 9,
BC041304
                                                                                                                                                                                                                                                                                                                               aGlyCysIleGlyAlaLeuArgGluAsnThrPheLeuLeuLysPhePheSerValPheLe 100
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Xenopus laevis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;

Xenopodinae; Xenopus.

1 (bases 1 to 1685)

Klein, S. and Strausberg, R.
                                                                                                                                         135 ATGCCCGGCAAGCATCCAGGACCCTGAGGTTGGCTGCTGCGGGAAATACTTT
                                                                                                                                                                                                                                               100 uGlyLeullePhePheLeuGluLeuAlaThrGlyIleLeuAlaPheValPheLysAspTr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Met ProGlyLysHisGlnHisPheGlnGluProGluValGlyCysCysGlyLysTyrPhe
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            1567
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Matches:
Conservative:
Mismatches:
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Gaps:
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          5.36e-73
955.50
85.11%
82.13%
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Alignment Scores:
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APO53455 1408 bp DNA linear PRI 03-NOV-1998
Homo sapiens tetraspan TM4SF (TSPAN-5) gene, complete cds.
APO53455
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                                                                                                                                                                                                                                                                                                                                                                     GlyCyslleGlyAlaLeuArgGluAsnThrPheLeuLeuLysPhePheSerValPheLeu 100
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Todd,S.C., Doctor,V.S. and Levy,S.
                                                                                                                                                                                                                          388 ATGTCCGGGAAG-----CACTACAAGGGTCCTGAAGTCAGTTGTTGCATCAAATACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                      GlyLeullePhePheLeuGluLeuAlaThrGlylleLeuAlaPheValPheLysAspTrp
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                                                                                                                                                                                                                                                              41 TrpAlaTrpGlyGluLysGlyValLeuSerAsnileSerAlaLeuThrAspLeuGlyGly
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                                          Length:
Matches:
Conservative:
Mismatches:
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Homo sapiens
                                                    944.50
83.76%
76.07%
73.62%
                                                  rercent Similarity:
Best Local Similarity:
Query Match:
DB:
                               Scores:
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LOCUS
DEFINITION
ACCESSION
VERSION
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Pred. No.:
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GVLSNISSITDLGGFDPVWLFLVVGGWMFILGFAGCIGALRENTFLLKFFSVFLGIIF
FLELTAGVLAFVFKOMIKDQLYFFINNNIRAYFDDIDLGNLIDFTQEYWQCCGAFGAD
DWNLNIYFNCTDSNASRERCGVFFSCCTKDPAEDVINTQCGYDARQKFEVDQQIVITT
KGCVPFEKHLQDDTTVVAGFFIGIALLQIFGICLAQNLVSDIEAVRASW"
                                                      120
                                                                                                   IleargaspGlnLeuAsnPhePheIleAsnAsnAsnValLysAlaTyrArgAspAspIle 140
                                                                                                                                                                                                         473
                                                                                                                                                    AspLeuGlaAsnLeu1leAspPheAlaGlnGluTyrTrpSerCysCyyAlaArgGly 160
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Garcia-Frigola, C., de Lecea, L. and Soriano, E.
Mouse Tspan-5 CDNA cloning
Wouse Tspan-5 CDNA cloning
Unpublished
(bases 1 to 3175)
Garcia-Frigola, C., de Lecea, L. and Soriano, E.
Garcia-Frigola, C., de Lecea, L. and Soriano, E.
University of Barcelona, Av. Diagonal 645, Barcelona 08028, Spain
Location/Qualifiers
superfamily"
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388. 1194
/gene="Tspan5"
/note="member of transmembrane /
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="tetraspanin Tspan-5"
/protein_id="AAF28869.1"
/db_xref="G1:6841033"

    3175
/organism="Mus musculus"
/mol_type="mRNA"
/strain="Swiss Webster/NIH"

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1. .3175
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PRI 29-SEP-2000
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Published Only in DataBase (2000)
2 (bases 1 to 4445)
Chara,O., Nagase,T., Kikuno,R. and Okumura,K.
Direct Submission
Submitted (24-AUG-2000) Osamu Ohara, Kazusa DNA Research Institute,
Department of Human Gene Research, 1532-3, Yana, Kisarazu, Chiba
292-0812, Japan (E-mail:odhainfo@kazusa.or.jp,
URL:http://www.kazusa.or.jp/NBDO, Tel:81-438-52-3913,
Fax:81-438-52-3914)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-and one pass sequencing and clone selection: Kazusa DNA Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 ArgCysGlyValProPheSerCysCysValArgAspProAla----MetSerSerThrPr 199
                                                                                                                                                                         oSerValAlaMetMetSerGlySerAsnTrpSerTrpSerSerArgAlaProTyrThrPr 219
                                                                                                                                                                                                 934 CAGTGTGGCTATGATGCCAGGCAAAAACCAGAAGTTGACCAGCAGATTGTAATCTACACG 993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. I (bases 1 to 4445)
Ohara,O., Nagase,T., Kikuno,R. and Okumura,K.
The nucleotide sequence of a long cDNA clone isolated from human
                                                                                                                   ProAsnAspTrpAsnLeuAsnIleTyrPheAsnCysThrAspLeuAsnProSerArgGlu
                                       GCIGATGATTGGAACCTAAATATTACTTCAATTGCACAGATTCCAATGCAAGTCGAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="For this clone, GeneMark analysis triggered an alert for spurious CDS split. The result of GeneMark analysis of the nucleotide sequence of this clone is accessible through http://www.kazusa.or.jp/NEDO.
                                                                                                                                                                                                                                                                                                                                                         AKU24427
Homo sapiens mRNA for FLJ00016 protein, partial cds.
AK024427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="spleen"
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fis (full insert sequence).
Homo sapiens (human)
Homo sapiens
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NYFWCTDSNASRERGGVPFSCCTKDPAEDVINTQCGYDARQKPEVDQQIVIYTKGCV
PQFEKRUQDNLTIVAGIFIGLALQIFGICLAQNIVSDIEAVRASW"
354 c 384 g 345 t 16 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LeuPheGlyPheAsnIleValPheTrpValLeuGlyAlaLeuPheLeuAlaileGlyLeu 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 Met ProglylyshisglnHisPheGlnGluProGluValGlyCysCysGlyLysTyrPhe
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         tetraspanin/TM4SF family
Biochim. Biophys. Acta 1399 (1), 101-104 (1998)
88390278
9714763
2 (bases 1 to 1408)
Todd,S.C., Doctor,V.S. and Levy,S.
Direct Submission
Submitted (12-MAR-1988) Medicine, Stanford, 300 Pasteur Stanford, C. Location/Qualifiers
Sequences and expression of six new members of
                                                                                                                                                                                                                                                                                                     /gene="TSPAN-5"
352. .1146
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/note="transmembrane 4 superfamily"
/codon_start=1
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/organism="Homo gapiens"
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BASE COUNT	890 a	ઠે	152 152
Alignmen	. 987000	අු	1020 CATTTATACTATGTTTTGGCCTCTGTGTATATAGAGTTTAGACCCCTGATGGAAGGTCTG 1079
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Percent	milarity: 25.33\$ Conserv.	q	1080 CCCTCAAACTTGCAAACTTAACCCCAGTGAAGAGCAGCCAGAGAAGAGTTCCTGAAACCC 1139
Query Match:	66.52% Indels:	ò	152 152
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3 8	ATGCCCGCCAAGCACCAGCA	qq	1200 ACACTGTCACCCACAGTCACCCACACCTAGTCACACACCACGCAGCACACTTGATCAC 1259
ò	21 LeuPheGlyPheAsnIleValPheTxpValLeuGlvAlaLeuPheLeuAlalleGlyLeu	ò	152 152
: A	CIGITIGECTICAACATIGECTICTGGGGGGGGCCCGGTTCCTGGCTATCCGCCTC	QQ	1260 ACCTACACCTACACATGGTCCCACAGTCACATGAGTCACACCCGATCACACCCCACACA 1319
ò	vGly	ò	152 152
q		Ωp	1320 CGGCGACAGGCCCTTGGCACCATTCACCACGAGAGTCAGCTCTGGATCCAGAGGTGAAG 1379
ò		ò	152 152
da		qΩ	1380 CAGAGCIGGIGCCTGCTICAAGCAGCICTCAACCCAGGGCAGAGGCAGACATAGCCAGGC 1439
'n	81 GlyCyslleGlyAlaLeuArgGluAsnThrPheLeuLeuLysPhePheSerValPheLeu 100	ò	152 152
Dp	CATTGGGGCCCTCCGGGAGAACACCTTCCTGCTCAAGTTTTTCTCCCGTGTTCCTC	QQ	1440 AGTTATGATGCAGTTCATTCATTCAGCACAGGATTGTTAAGGGCCTACCATATGCC 1499
'n	101 GlyLeuIlePhePheLeuGluLeuAlaThrGlyIleLeuAlaPheValPheLysAspTrp 120	ò	152 152
QQ		qq	1500 GGACCCAGAGCCCTGAGGATTCGGCGGGAAGAAGCTGGGACCTGTCCTCTCAG 1559
ó,	121 ileArgAspGlnLeuAsnPhePheIleAsnAsnAsnValLysAlaTyrArgAspAspIle 140	ò	152 152
QQ		qa	GGCTGGCAGTCGGGAAGAGACAGATGGTGAACAAGCAGAACAAACA
ò	141 AspLeuGlnAsnLeuIleAspPheAlaGlnGluTyr	ð i	
DÞ	540 GACCTCCAGAACCTCATTGCTCAGGAATACGTGAGTCCAGTGTCCAGCCTGGGA 599	Q O	Catacgtgtgtatgcaaaattgtacattgtggtaagagtcaaaatgaagggtggagatg
ó	152 152	ò	
Dp	600 CACCTGTAGGAGGCGCCTTCCTGGCAGAATGAGGAAGCAAGTTCCCTGTGATGGGAC 659	q	1680 GGAAGGCCTCTGCGTGGAGAGCTTGAAGCCTCCCAAAGGAGGAGAAGGAAG
ò	152 152	ò	152 152
Dp	660 CATCTTCCTTACCCACCTGGGCTAGCGGGCCCCAGGAGAGAGA	셤	1740 AGTGTTCTGTAGCAGCAGCAGCTGGCGCTGAGCAGGCCAGGAGGCAGGTGCAGGCTGA 1799
γ	152 152	ð	152 152
DP	720 CGAGGAGAGCCAGCCCTGCTGATCCTTATGGGTCCCCATTTGCCTAGTGCCATAGGGCC 779	qa	1800 GCCCTGCCCTGGGACCAGCACATGCAGGCATGTGGCAGGCCTGACTCCTCCAGCTCTCT 1859
ò	152 152	δ	152 152
DÞ	780 ACGGCCTTGGGAAACAGAGGCACGGGCTCCACACTAGCAGCTCCCAGGCCAGGGCCTAC 839	ପ୍ର	1860 GGCTCGGCCACGGGGCCTGCCTGTGTCTGCTGCCGAGCTTGAGCTCCCCCAGCCCTGTGG 1919
γ̈́	152 152	ò	152 152
qa	840 GACACACGGGGAGAATGGGGGAAATGTGGACATAAAATATAGATTTCTACTTCTGGTAAACC 899	셤	1920 GCTGCTCTCCAGCCCCTGCGGCTGCTCAGTGAGGGCTGTGTGCACCCGTGTGCCCCCAC 1979
γ̈́ο	152 152	È	152
ପୁ	900 TIGGGCCCACGGTATIGGCTGCAGCTAIGTIGCTGCTGCCCTTCACTGGTACAGAGGCT 959	셤	1980 AAGACCATGGTTCATGGCAGATCCCAAACTCGCCATTGCTCCTGCCTAGGGGACAGCTTA 2039
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GlyLeuilePhePheLeuGluLeuAlaThrGlyIleLeuAlaPheValPheLysAspTrp 120
                                                                       PC C12N15/09,C12P21/02,C12Q1/68,A61X37/02,C12N5/00,C12N15/00 CC Secretory proteins and polynucleotides encoding the same FH Key Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lleArgAspGlnLeuAsnPhePheIleAsnAsnAsnValLysAlaTyrArgAspAspIle 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProAsnAspTrpAsnLeuAsnIleTyrPheAsnCysThrAspLeuAsnProSerArgGlu 180
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CO7K14/47, A61K38/00, A61P43/00, C12N1/15, C12N1/19, C12N1/21, C12N5/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           590 GATTTGCAAAACCTCATAGACTTCACCCAGGAATATAT-TCC--------
PI DAVID MERBERG, MAURICE TREACY, MICHAEL J AGOSTINO, ROBERT STEININGER II
                                                                                                                                /organism='Homo sapiens (human)'.
Location/Qualifiers
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Matches:
Conservative:
Mismatches:
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/mol_type="genomic DNA"
/db_zref="taxon:9606"
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Secretory proteins and polynucleotides encoding the same.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1110)
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PF 18-FEB-1999 JP 2000532422
PR 18-FEB-1999 US 60/075038,17-FEB-1999 US 09/251600 PI
KENNETH JACOBS,JOHN M MCCOY,EDWARD R LAVALLIE,LISA A COLLINS PI
RACIE,
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                                                                                                 2160 GCTTTGTAGAACCTCTGGGGCAAGTGTGGGAGGCCTGCTGCAGACATGGGGCCCAGCGGT
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JP 2002504488-A/2
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Homo sapiens (human)
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VIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapba-ramail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
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                                                                                                                                                  ROD 16-APR-2003
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                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1. (baees 1 to 2428)
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Submitted (06-MAR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                            expressed, mRNA
                                                                                                                                               SC025568 2428 bp mRNA linear dus musculus DNA segment, Chr 14, ERATO Doi 226, ex (CDNA clone MGC:36595 IMAGE:5322531), complete cds.
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        822 GCTGATGATTGGAACCTAAATATTTACTTCAATTGCACAGAAT
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/noTe="NBT-4 oligonucleotide used in cell proliferation assay on SM620 cells"
229 c 249 g 224 t
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Compositions and methods for treating neoplastic disease using :
-4 modulators
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766 AAGGCTGTGTGCCCCAGTTTGAGAAGTGGTTGCAGGACA 805
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Conservative:
Mismatches:
Indels:
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CHIRON CORPORATION (US)
LOCATION/Qualifiers
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Seguence 1 from Patent WO0198350.
AX343015
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Maus musculus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1. (basea 1 to 2498)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B. Buetcow, K.H., Schaefer, C.F., Bhar, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S. I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
Worley, K. C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Vilalon, D.K., Wanny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ROD 16-APR-2003
                               591
                                                                            ArgGluArgCysGlyValProPheSerCysCysValArgAspProAlaMet-SerSer-- 197
                                                                                                                                                                                                           592 CGAGAGAAATGTGGGGTACCCTTCTCCTGCTGTGTGCCCAGATCCTGCAAAAAGTCGT 651
                                                                                                                                                                                                                                                                                                                                                                             112 TTTACAAAAGGATGCATCCAGGCTCTGGAAGGCTGCCCCAGGAACA---TCTACATT 768
                                                                                                                                                                                                                                                                                                                                       -------SerAsnTrpSerTrpSerSerArgAlaProTyrThrProLysAlaVa 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BCO24611
2498 bp mRNA linear ROD 16-APR-20
Mus musculus DNA segment, Chr 14, ERATO Doi 226, expressed, mRNA
(cDNA clone MGC:28503 IMAGE:4188261), complete cds.
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   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                             222 lTrp-----AlaSerLeuArgSerGlyCys 230
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AUTHORS
TITLE
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DWDLNVYFNCSGASYSREKCGVPFSCCVPDFAGKVVNTQCGYDVRIQLKSKWDEFIFT
KGCIQALEGWLFRNIYITAGASYSREKGGYFAISLLQIFGIFLARTLISDIBAVKAGHHF"

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                                                                            found
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Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
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| fmol Lype="mRNa"
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| folone="MGC:28503 IMAGE:4188261"
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                                                                    Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: TRAK Plate: 37 Row: e Column: 12 This clone was selected for full length sequencing because it passed the following selection criteria: GenomeScan gene prediction, Similarity but not identity to protein.
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Indels:
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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I. I., W.B., Gruber, C., Jessee, J. and Polayes, D.

Pull-length cDNA libraries and normalization

Unpublished

On Feb 13, 2001 this sequence version replaced gi:12791995.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedax - France

Email: seqrefégenoscope.cns.fr Web: www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 3528.f For

more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CSODC029DE05QPl&cluster=3528.f. Contact :

Feng Liang Email: fliang@lifetech.com URL:
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Copyright (c) 1993 - 2003 Compugen Ltd.
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http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSODC029DE05QP1. Location/Qualifiers
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Was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
http://www.genoscope.org.fr
ttp://www.genoscope.org.fr
egi-bin/cluster.cgi?seq=CSODD005DA10QD1&cluster=3528.f. Contact :
Frog Liang Email : fliangaliferech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODD005DA10QP1.
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/clone_lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
331 c 336 g 253 t 37 others
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GGCCAGTTTGAGAAGTGGCTGCAGGACAACCTGATCGTGGTGGCTGGGGTCTTTTGTGGGC
                                                         GGCCAGTTTGAGAAGTGGCTGCAGGACAACCTGATTGTTGTTGTGGGGGGGAGTCTTCATGGGC
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Pred. No. 1.5e-93;
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DD005YB20"
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Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Arakawa,T., Ishai,R., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Gojobori,T., Boro,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Kadota,K., Matsuda,Y., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,I., Fuzuki,R., Tomita,M., Baldarelli,R., Barsh,G., Blake,J., Bofffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmanni,M., Hume,D.A., Kamaya,M., Lee,N.H., Lyons,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,J., Sakamoco,N., Sasaki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S., and Hayashizaki,Y.
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L Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
                                                                                                                                                                  Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, W., Komo, H., Okazaki, Y., Murametsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length CDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
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Nature 409 (6821), 685-690 (2001)
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                                                             cloning
                                     Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA Meth. Enzymol. 303, 19-44 (1999) 99279253
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AKO08761. GI:12843154
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Mus musculus (house mouse)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                       294 GAGAAGGGCGTTCTCTCGAACATCTCAGCGCTGACAGAWCTGGGAGGCCTTGACCCGTG
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(FRAGMENT) homolog [Homo sapiens] (SPTR|Q9UKB9, evidence:
FASTY, 86.9%ID, 99.1%length, match=363)
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                                                                                                                                   Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
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Genoscope - Centre National de Sequencage
BP 191 91006 EWRY cedex - France
Email: seqref@genoscope.cns.fr. Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3528.f For
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Musualia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Massulus
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Rammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Rokazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
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Rakawa, T., Plukda, S., Hara, A., Hashizume, M., Imotani, K., Ishimagawa, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunish
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BY708665.1 GI:27119857
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URL.http://genome.gsc.riken.go.jp/
Adachi.J. Aizawa.K. Akimura.T., Arakawa,T., Carninci.P., Fukuda AGchi.J., Aizawa.K., Akimura.T., Historane,T., Hori,F., Imotani,K., S., Hashizume,W., Hayashida.K., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y., Kondo,S., Konno
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/organism="Homo sapiens"
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/mol type="mRNA"
/do Xref="Lexan:9606"
/clone="CSODIO05YM07"
/tissue type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
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279 c 288 g 205 t 9 others
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more information about this cluster, see http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi/seg-cSoD1005AG04QP1&cluster=3528.f. Contact
Feng Liang Email : fliang@lifetech.com URL :
http://fullengfh.invitrogen.com/ InVitroden Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOD1005AG04QP1.
Location/Qualifiers
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Pred. No. 6.3e-83;
); Mismatches 66; Indels
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Matches 813; Conservative
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi, Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi, Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

18 1 (bases 1 to 938)

19 NIH-MGC http://mgc.nci.nih.gov/.

10 Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Clone distribution: MGC clone distribution information can be http://image.llnl.gov

Plate: LLOM2885 row: j column: 16

High quality sequence stop: 649.
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AGENCOURT 10475185 NIH_MGC_107 Homo sapiens cDNA clone IMAGE.646576 5', mRNA sequence.
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                                                                                                                                                                                                Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA computer based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K.,
Numazaki,R., Ohno,M., Ohaeto,N., Satio,R., Sakazume,N., Sano,H.,
Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Takeda,YI.
Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
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Please visit our web site (http://genome.gsc.riken.go.jp) for
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/dev_stage="adult"
/lab_host="SOLR"
stomach:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="2210021G21"
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BE615772

849 bp mRNA linear EST 24-AUG-2000 601279927F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3621871 5', mRNA sequence.
BE615772.1 GI:9897371
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/lab_nost="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_39"
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Site_2: EcoRI; cDNA made by oligo-dT priming.
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into BcoRI/AhoI sites using the following S' adaptor: GGGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
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WIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contract: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM296 row: e column: 08
High quality sequence stop: 699.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                   GGCC - - AGTTTGAGAAGTGGCTGCAGG
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241 c 2
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Homo sapiens
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TITLE
JOURNAL
COMMENT
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                                                                                                                                                                                 /note=Torgan: breast; Vector: poTB7; Site 1: EcoRI; Site 2: XhoI; cDNA made by oligo-dT priming.
Site 2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACCAGG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of Galifornia, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65 GGCCTGGCTCCCGGCTCCGGTTTCCGGGCGGCGGCGGCGCTCACCATGCCCGGCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAGAAGGGTGTTCTCCAACATCTCTGCGCTGACCGATCTGGGAGGCCTCGACCCTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AACATTGTTTTCTGGGTGCTGGGAGCCCTGTTCCTGGCCATCGGCCTCTGGGCCTTCGGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26.2%; Score 663.8; DB 13; Length 938; larity 91.4%; Pred. No. 3.8e-79; Conservative 0; Mismatches 62; Indels 7;
/organism="Homo sapiens"

"Mol type="mRNA"

db xref="taxon.9606"

/clone="IMAGE:6646576"

/tissue_type="adenocarcinoma, cell line"

/lab host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_107"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
les 738; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                          162
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/clone="IMAGE:5441687"
/tissue_type="astrocytoma grade IV, cell line"
/lab.host="DHIOB (phage-resistant)"
/clone lib="NIH MGC 98"
/clone lib="NIH MGC 98"
/note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI: cDNA made by oligo-dT priming. Directionally
cloned into EcoRI.XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superecript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  488 ATCTACTTCAACTGCACTGACTTGAACCCCCAGCCGGGGGGGCGCTGCGGGGGGGCCTTCTCCC
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                                                                                                                                                                                                                                                    Length 1032;
                                                                                                                                                                                                                                                  Score 632.2; DB 12; Length
Pred. No. 5.6e-75;
0; Mismatches 73; Indels
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                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 82.5%;
Matches 804; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               137
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BMS63474 GI:18810427
EST.
                                                                                                                                                                                                                                                                   626
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Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1032)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCs
cDNA Library Preparation: Rubin Laboratory
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://fmage.llnl.gov
Plate: LLCM1916 row: f column: 24
High quality sequence stop: 697.
      CCTTCCTGCTCAAGTTTTTTCTCCGTGTTCCTCGGTCTCATCTTCTTCCTGGAGGCTGGCAA
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/db_xref="taxon:9606"
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/lab host="EMDH10B"
/lab host="EMDH10B"
/cloin lib="WAPCL"
/cloin lib="WAPCL"
/note="Vector: pCWV-SPORT6; Site_1: EcoRV; Site_2: Not I;
/note="Vector: pCWV-SPORT6; Judg, kidney and muscle.
Subtracted with brain, liver, lung, kidney and muscle.
Directionally cloned. Priming method: oligo-dT. Average insert size: 1800 bp. Library amplification: 26,000 fold.
Kristi A. Egland, James J. Vincent, Robert Strausberg, Bungkook Lee & Ira Pastan: Discovery of new breast cancer genes encoding membrane and secreted proteins.
Manuscript submitted."
                                                                                                                                                                                                                                                                                                          901 bp mRNA linear EST 12-NOV-2002
10735735 MAPCL Homo sapiens CDNA clone IMAGE:6722499 5',
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/db_xref="taxon:9606"
/clone="INAGE:6722499"
/cell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231, hTERT-HME1
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NIH-MGC http://mgc.nci.nih.gov/.

NiH-MdC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished

Contact: Robert Strausberg, Ph.D.
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                                       GGGCCAGTTTGAGAAGTGGCTGCAGGACAACCTGATCGTGGTGGCTGGGGTTTTTTTGTGGG
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Tissue Procurement: Kristi A. Egland, Ira Pastan
Tissue Procurement: Kristi A. Egland, Ira Pastan
CDNA Library Preparation: Invitrogen Corporation
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can I
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14285 row f column: 03
High quality sequence stop: 683.
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Pred. No. 3.2e-73;
0; Mismatches 53; Indels
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                                                   /dlone=TMAGE:463999"

/tissue_type="melanotic melanoma"

/tab_host="mulua" (page_resistant)"

/clone lib="NHIM (GC 20"

/clone lib="NH MGC 20"

/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoR1; cDNA made by oligo-dT priming. Directionally
cloned into EcoR1/XhoI sites using the following 5'
adaptor: GGCAGGGG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies)."

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86.2%; Pred. No. 1.7e-73;
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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BX447619 Homo sapiens B CELLS (RAMOS CELL LINE) Homo sapiens CDNA clone CSODG006YC20 5-PRIME, mRNA sequence.

BX447619.1 GI:31025857
EST.
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Homo sapiens
Homo sapiens
Bukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukampalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Full Homorphished
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Bmail: Begrafégenoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3528.f For
http://www.genoscope.cns.fr/
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOAGGO6BB10QP1&cluster=3528.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
                                                                                                                                TTCCTGGAGCTGGCAACAGGGATCTTGGCCTTCGTATTCAAGGACTGGATTCGAGACCAG
                                                                                                                                                                                                                                                                                                    AACCTCAATATCTACTTCAACTGCACTGAACTTGAACCCCAGCGGGAGCGCTGCGGGGTG
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TITLE
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B1914325 717-OCT-2001
603182305F1 NIH MGC_121 Homo sapiens CDNA clone IMAGE:5246304 5',
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Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI1621 row: j column: 01
High quality sequence stop: 712.
Location/Qualifiers
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AGAAGGGTGTTCTCCCAACATCTCTGCGCTGACCGATCTGGGAGGCCTCGACCCTGTGT
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Contact: Robert Strausberg, Ph.D.
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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// forgatism="mcmuc sapiens"
// forgatism="mcmuc sapiens"
// folone="Imbas: 483979"
// folone="Imbas: 483979"
// folone="Organ: prosetter vector: pDNR-LIB (Clontech);
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                                                                        781 bp mRNA linear EST 15-MAY-2001
602719148F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:4839779 5',
BG770931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1669 row: o column: 12
High quality sequence stop: 697.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 781)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCAGCACTTCCAGGAACCCGAGGTCGGCTGCTGCGGGAAATACTTCCTGTTTGGCTTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              176 t
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/organism="Homo sapiens"
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                                                                                                                                                                                                                     BG770931.1 GI:14081584
EST.
                                                                                                                                                                                                                                                                              Homo sapiens (human)
Homo sapiens
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239 c
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Best Local Similarity
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VERSION
KEYWORDS
SOURCE
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                                                      RESULT 13
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/organiam="Homo sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
/db_txef="taxon:9606"
/clone="Infags:4643959"
/tissue_type="melanotic melanoma"
/lab host="mB10B (phage-resistant)"
/clone=lib="NIH MGC20"
/clone=lib="NIH MGC20"
/note="Organ: skin; Vector: pOTB7; Site 1: Xho1; Site 2: EcoR1; cDNA made by oligo-dT priming. Directionally cloned into EcoR1/Xho1 sites using the following 5' adaptor: GGCACGGG(G). Size-selected >500bp for average innert size 1:8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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                                                               Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72 AICCCGGC-CCCGGCTCCCGGGTCCCGGGCGGCGGCGCTGCTCACCATGCCGGCCAGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148 CACCAGCATTTCCAGGAACCTGAGGTCGGCTGCTGCGGGAAATACTTCCTGTTTGGCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    370 GGCTCTCCGGGAGAACACTTTCCTGCTCAAGTTTTTCTCAGTGTTCCTTGGCCTCATCTT
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                                                  Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleos Mammalia; Eutheria; Primates; Catarthini; Hominidae; Homo.

I (bases I to 902)

NIH MGC http://epoc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MC Unpublished Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Arcc/Crp/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyre Genomics, Inc.
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://inage.llnl.gov
Plate: LLCM1414 row: p column: 08
High quality sequence stop: 813.
                                                             Craniata; Vertebrata; Eutele
Catarrhini; Hominidae; Homo.
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          Homo sapiens (human)
Homo sapiens
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AUTHORS
TITLE
JOURNAL
COMMENT
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Site 2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon 0.10ning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIM MGC Library."
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BG478644 GI:13410923
EST.
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                                                                                                                                                                                                                                                                                                      Query Match
23.7%; Score 602.4; DB 12; Length 718;
Best Local Similarity 91.3%; Pred. No. 6.3e-71;
Matches 639; Conservative 0; Mismatches 61; Indels 0;
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Human secreted pro Novel human cDNA s Human TANGO 339 cD Human TANGO 339 KI Human TANGO 339 FZ Human TANGO 339 FZ Human TANGO 339 FZ Human TANGO 339 A4

Human tetraspan pr DNA encoding novel Human tetraspanin-Polynucleotide seq Human cDNA encodin

Clone HEBEJ16 codi Clone HEBEL16 codi CDNA sequence #126

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Database

us-09-972-970-2.rng

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Human TM4SF receptor-encoding gene 1 cDNA clone HOFOB55, SEQ 1D NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; 4-transmembrane superfamily; TM4SF receptor; breast cancer; ovarian cancer; immune disorder; Addison's disease; wound healing; gene therapy; autoimmune branchitie; anaemia; autoimmune thyroiditis; diabetes mellitus; allergy; Crohn's disease; multiple sclerosis; rheumatoid arthritis; ulcerative colitis; cardiovascular disorder; myocardial ischaemia; neurological disease; antifungal; antiviral; antiparasitic; cancer; ss.
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/product= "Human TM4SF receptor protein"
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Human 23228 CDNA.
Clone HNTMH27 codi
Human polynucleoti
Rat gamma-hydroxyb
Human EST-derived
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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         GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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18-OCT-2001

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2 4 4 5 9 7 8

Score

Result No.

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SCI INC
  10-APR-2000; 2000US-195336P
       (HUMA-) HUMAN GENOME
                 WPI; 2002-017447/02.
P-PSDB; AAE13218.
            Ruben SM;
            Shi Y,
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Novel isolated protein, a member of 4-transmembrane superfamily of receptor polypeptides, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases

Claim 1; Page 265-266; 271pp; English

The invention relates to human 4-transmembrane superfamily (TM4SF)
receptor polypeptides and polynucleotides. Sequences of the invention
are useful for preventing, treating, ameliorating or diagnosing a
pathological condition or a susceptibility to a pathological condition.
TM4SF polypeptides are useful for screening molecules which modify
their activity. TM4SF mucleic acids, protein, antibodies, agonists and
antagonists are useful in the diagnosis, treatment and prevention of
cancer, particularly breast and ovarian cancer, and other cancers of
the adrenal gland, bone, bone marrow, breast gastrointeestinal tract,
liver, lung, or urogenital; immune disorders such as Addison's disease,
allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
alaberes mellitus, Crobin's disease, multiple sclerosis, rheumatoid
archritis and ulcerative colitis; cardiovascular disorders such as
cerebral anoxia and epilepsy; and infectious diseases such as
cerebral anoxia and epilepsy; and infectious diseases such as
cerebral anoxia and epilepsy; and infectious diseases such as
cerebral anoxia and epilepsy; and present sequence is human TM4SF
receptor protein encoding CDNA.

Sequence 2538 BP; 528 A; 669 C; 747 G; 594 T; 0 other;

ö 120 120 180 180 240 240 300 300 360 CTGCATCGGGGCTCTCCGGGAGAACACTTTCCTGCTCAAGTTTTTCTCAGTGTTCCTTGG 420 480 420 9 9 CCACGCGTCCGGCCGCGGGCCCCGGGCTAGGCCCCGGGCGGCCTCTAGCCCCAGGGCGGCCCC GTGGAGGCCGATCCCGGCCCCCGGTTCCCGGGCCGGCGGGGGGCGCTGCTCACCAT GTTTGGCTTCAACATTGTTTTCTGGGTGCTGGGAGCCCTGTTCCTGGCCATCGGCCTCTG CGACCCTGTGTGGCTGTTTGTAGTGGTTGGAGGCGTCATGTCCGTGCTGGGCTTTGCCGG CTGCATCGGGGCTCTCCGGGAGACACTTTCCTGCTCAAGTTTTTCTCAGTGTTCCTTGG CCACGCGTCCGGCCGCCGCCGGGCTAGGCCCCGGGCGCTCTAGCCCAGGGCGGCCC GCCGGGCAAGCACCAGCACTTCCAGGAACCCGAGGTCGGCTGCTGCGGGAAATACTTCCT GTTTGGCTTCAACATTGTTTTCTGGGTGCTGGGAGCCCTGTTCCTGGCCATCGGCCTCTG GGCCTGGGGTGAAAGGGTGTTCTCTCCAACATCTCTGCGCTGACCGATCTGGGAGGCCT 241 GGCCTGGGGTGAGAAGGTGTTCTCTCCAACATCTCTGCGCTGACGGATCTGGGAGGCCT CCTCATCTTCTTCCTGGAGCTGGCAACAGGGATCTTGGCCTTCGTATTCAAGGACTGGAT Gapa , , Query Match 100.0%; Score 2538; DB 24; Length 2538; Best Local Similarity 100.0%; Pred. No. 0; Marches 2538; Conservative 0; Mismatches 0; Indels 0; Н 61 121 181 181 301 301 361 361 421 421 셤 ઠ ò a g g a ò õ ò ઠે g ò 셤 ò

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Human; transmembrane protein; cell proliferation disorder; myeloma; reproductive disorder; smooth muscle disorder; neurological disorder; arteriosoclerosis; leukaemia; acquired immunodeficiency syndrome; AIDS; allergy; ovulatory defect; angina; hypertension; stroke; epilepsy; Alzheimer's disease; Tourette's disorder; ss.
                                                                                                                                                                                                                                                                                                                                     New human transmembrane proteins are used to treat a disease condition associated with decreased expression of functional Tourette's disorder, angina and leukaemia -
                                     encoding a human transmembrane protein.
                                                                                                                                  Location/Qualifiers
113..1102
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99US-0139565
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                    (first entry)
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P-PSDB; AAB18969.
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                   08-FEB-2001
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Baughn

Bandman O,

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Hillman JL, J;

e.g.

or HTMP

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The present sequence encodes a human transmembrane proteins (HTMP). Agonists and antagonists of the protein are used to treat a disease or condition associated with overexpression of the protein. Diseases and conditions which can be treated include cell proliferative, immunological, reproductive, smooth muscle and neurological disorders e.g. arterlosclerosis, myeloma, leukaemia, acquired immunodeficiency syndrome (AIDS), allergies, ovulatory defects, angina, hypertension, stroke, Alzheimer's disease, epilepsy and Tourette's disorder. The polymucleotides may be used to detect and quantify gene expression in biopsied tissues where protein expression may be correlated with disease e.g. to determine absence, presence or excess expression of HTMP or to monitor regulation of HTMP expression during therapeutic intervention.
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40.1%; Score 1019; DB 21; Length 2091;
Best Local Similarity 76.6%; Pred. No. 3.3e-236;
Matches 1544; Conservative 0; Mismatches 365; Indels 106;
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Claim 4; Page 113-114; 130pp; English
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Db 1240 AAGTGCCGCCTGAGCCTTGTACATAGGAGCTGGCCTCCCACCTCTGCAGGCTTATTT 1297 Qy 1316 CCTGCAAATGCTGCAGCCTGTGGGCCAAGCCCGGATCGAAGCGTGAAGA 1375 Db 1298 CCTGCACCTCGAGGCCGCTGCGGCCAATCTGGAGTGAAAAGAGGTCTGGAGGTTGAAGG 1353 Qy 1376 ATTGGGGAGGCTGGAGCCTGCCCAAAAGAGGCCTGGAAGGCTCGCCTCCT 1435		Oy 1496 GGAAGGTTTTGGGCAGGACGTAGCTGGAAGCTTGTCACCCATGGGGAG 1555 D		QY 1676 CCTGGGTCTGCCTTTCCTAGGACAACCCCAGTACAGCCCTGTGCCTGTGCTCCA 1735	Db 1672 -CCTGCTACTACTGGGGTTTGGAGATTTCTCAGAGCCAACTGG 1728 Qy 1796 CTCAGATTGGGGAAGCCTGGTGTTCTCAAATGCGAAAAGCGTGTGT-TGGAG 1854	OY 1855 TAITTGTGAATCAAAGGAGAGGTTTGGCCTAGTGCCCAGTCTTTAACTTAGA 1907	QY 1908 TGCCTCAGGGCTGGGTTATAAAAATAAAGTAGGCCTTTGAGCTGTGAGGCC 1963	1909 SULT 3 190838 ABL90838	AC ABL90838; XX XX DT 24-MAY-2002 (first entry)	Human polynucleotide SEQ ID NO 1400. Cytostatic; immunosuppressive; nootropic;	<pre>KW antiallergic; heparotropic; antidiabetic; antiinflammatory; antiulcer; KW vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; KW cardiant; gene therapy; cancer; immune disorder; cardiavascular disorder; KW neurological disease; infection; human; secreted protein; gene; ss.</pre>	Homo sapiens. WO200190304-A2.	XX PD 29-NOV-2001. XX
1	311 GENERAL TIGHT	TTCCTGGAGCTGGCAACAGGGATCTTGGCCTTCGTATTCAAGGACTGGATTCGAGACCGG 4	431 CICATION TANCARCA CARGO CITATOR SECULD TO THE SECULD SECULD SECUNDARY TO THE SECUNDARY SECUN	611 AACCTCAATAICTATIICAACTGCACTGACTTGAACCCGAGCGGAGGGGGGGGG 670		GGCCAGTTTGAGAAGTGGCTGCAGGACAACCTGATCGTGGTGGCTGGGGTCTTTGTGGGG 84	847 ATCGCTCTCCAGATCTTGGTATCTGCCTGGCCCAGAACCTTGTGAGTGA		1027 GCCGTGCCGTCTGCCTGGGGCCCC-AGCCCAGACCCCTGCCAACATGTTTC-TTGG 1084 	1085 CCTGGGTAGTACGATGAGCCAACCTTTAAAACTTGGCATATTTCATGTAAAAGTCC 1144 	1145 AGATCCCCAGCATCTTGTGAAGAATGGCCATCCGGCCACAGGGCTCTTCTATGGCTTCG 1204 	1205 TCTCCTGGGATGTGCGCTTCCTGAGGGACCCACCCTCACCCGTGTCC 1258	1259TGCCTGCCTGACCTGGGAGCTGGCCTCCTCCACCTCTGCAAGTTTTTCC 1315

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                                                                                                                                                                                                                                                                                                                                            The invention relates to novel genes (ABL89449-ABL90853) and proteins (ABB89040-ABB90444) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune collits; (c) cardiovascular disorders such as myocardial ischaemias; collits; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and parasitic infections diseases such as viral, bacterial, fungal and parasitic infections diseases such as viral, bacterial, fungal and parasitic infections diseases such as viral, bacterial, fungal and parasitic infections diseases such as viral, bacterial, fungal corrections, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                             Claim 4; SEQ ID NO 1400; 2081pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37.4%; Score 948.4; DB 24;
82.1%; Pred: No. 3.6e-219;
tive 6; Mismatches 213;
                                                                           (HUMA-) HUMAN GENOME SCI INC
18-MAY-2001; 2001WO-US16450
                                      19-MAY-2000; 2000US-205515P
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Matches 1244; Conservative
                                                                                                                  Rosen CA;
                                                                                                                                                       WPI; 2002-122018/16.
P-PSDB; ABB90429.
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This sequence encodes tetraspanin 23228. This protein is a cell surface protein having four transmembrane domains (TM1-TM4). TM1, TM3 and TM4 have a single polar maino acid located within them, which may interact with each other amino acid located within them, which may interact with each other and contribute to domain stability. The cytoplasmic N-cand C-terminal domains and the intracellular loop between TM2 and TM3 and TM4 contains conserved Cys residues and may function to bind extracellular growth factors, such as HB-EGF, TGF-alpha and complex control comphiregulin. The 23228 protein is useful for diagnosing and treating amphiregulin. The 23228 protein is useful for diagnosing and treating such as diabetes mellitus, arthitis, multiple aclerosis, concephalomyelitis, dermatitis, Crohn's disease and asthma; cell metastasis, and/or viral infections. 23228 polypeptide can control cellular signalling activity, bind to an extracellular growth factor, for example, amphiregulin, regulate cell proliferation, bind to a cell surface protein, to recruit intracellular kinases, to regulate cell motility, bind to another tetraspanin such as CDB1, to association control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control contro
                                                                                                                                                                                                    Gene; tetraspanin; 23228; cell surface protein; transmembrane domain; extracellular growth factor; HB-EGF; TGF-alpha; amphiregulin; diabetes mellitus; arthritis; multiple sclerosis; encephalomyelitis; dermatitis; Crohn's disease; and asthma; cancer; metastasis; viral infection; cellular signalling activity; cell proliferation; cell motility; CD81; B-Cell antigen receptor; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New tetraspanin 23228 polypeptide useful in screening assays, predictive medicine and as a prophylactic or therapeutic agent, e.g. for hematopoietic and immune diseases such as diabetes or multiple sclerosis -
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
168..980
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/product= "23228"
AAI72633 standard; cDNA; 3185
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Score 790.4; DB 24; Length 3185; Pred. No. 7.8e-181;

31.1%; 92.3%;

Best Local Similarity

Query Match

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CGCGTCCGGCCGCAGCCGCCCCGGGCTAGGCCCCCGGGCGGCCGCCCAGGGCGGCCCGTG
                   CGCATGAAGCCGCAGCCGGCCCGGCTCCGGCGCGCCCTATAGCCCCAGGCCGCG
                                                       GAGGGCCGATCCCGGC-CCCGGCTCCGGTTCCCGGGCCGGCGGCGGCTGCTCACCATGC
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                          GAGAAGGGGTTCTCTCGAACATCTCAGCGCTGACACATCTGGGAGGCCTTGACCCCGTG
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                                                                      Gene therapy; human; 4 transmembrane superfamily receptor protein; addocrine; cardivosacular; cerebrovascular disease; neural disorder; reproductive; skin; renal system; autoimmune; hyperproliferative; ocular; bacterial infection; viral; fungal; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to isolated nucleic acids and proteins encoding human soluble 4 transmembrane superfamily receptor protein (see encoding human soluble 4 transmembrane superfamily receptor protein (see AAC90012-C90023 and AAB49502-B49513). The present sequence is one such nucleic acid. The present sequence is useful for preventing, traating or pathological condition e.g. endocrine disorders e.g. Addison's disease, (cardio) vascular diseases, neural disorders e.g. Addison's disease, erebrovascular diseases, neural disorders e.g. Alzheimer's and Parkinson's disease, reproductive disorders e.g. Alzheimer's and proviatis, renal system disorders e.g. nephitis, (auto) immune system disorders e.g. graft vs. host disease, hyperproliferative disorders e.g. neoplasms of the pancreas, ocular disorders e.g. glaucoma and infections caused by bacteria, viruses and fungi.
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                                    Clone HNTMH27 coding sequence
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03-UN-1999; 99US-0137797.
11-JUN-1999; 99US-0138573.
18-MG-1999; 99US-0149447.
28-JAN-2000; 2000US-0178770.
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(first entry)
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Best Local Similarity 92.6
Matches 850; Conservative
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Rosen CA;
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                                                                      CAGGAATATTGGTCTTGCTGCGGAGCCCGAGGGCCTAATGACTGGAACCTCAATATCTAT
                                                                                          CAGGAATACTGGTCTTGCTGCGGAGCCCCGAATGACTGGAACCTCAATATCTAC
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AACAACAACGTCAAGGCCTATCGGGATGACATTGACCTCCAGAACCTCATTGACTTTGCT
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/product= "gamma-hydroxybutyrate receptor"
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Collers in esequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO ce they way way.
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                                                                                                                                                                                                                                                   New polynucleotides comprising sequences assembled from expressed agguence tags (ESTS), useful for treating cell-proliferative, neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet or coagulation disorders
                                                                                                                        Zhao QA, 1
Ghosh M;
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Best Local Similarity 88.1%; Pred. No. 6.5e-177;
Matches 922; Conservative 0; Mismatches 91; Indels 34;
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                                                                                                                    Goodrich RW, Asundi V, Zha
Ma Y, Yamazaki V, Chen R,
J, Wang D, Drmanac RT;
               05-MAR-2002; 2002WO-US05095
                                                 05-MAR-2001; 2001US-0799451
                                                                                                                                      Yang Y, Ma
T, Wang J,
                                                                                                                                                                                               2002-759812/82
                                                                                      (HYSE-) HYSEQ INC.
                                                                                                                        Zhou P,
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Wehrman T,
                                                                                                                                                                                                                                                                                                                                           Claim 1;
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17-JUL-2000; 2000US-0617746.
03-AUG-2000; 2000US-06317451.
15-SEP-2000; 2000US-063870.
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Cao Y, Drmanac RA,
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                                                                                                                                                                                                                                                                               This sequence represents the CDNA sequence encoding a novel rat Gamma-hydroxybutyrate receptor (GHBR) isolated from rat brain hypocampal CC gamma-hydroxybutyrate receptor (GHBR) isolated from rat brain hypocampal CC cell cDNA library. The invention relates to the isolation of this novel sequence, fragments of it and homologues of the sequence except for those homologues that having GenBank accession numbers AAC 17120 (human CC tetraspan NET-4), AAG15405, AA967250 or A1467210. GHBR is the receptor CC tetraspan NET-4), AA6174505, AA967250 or A1467210. GHBR is the receptor CC tor gamma-hydroxybutyrate in the rat brain and is involved in regulating dopaminergic, opioid and GABA (gamma-aminobutyric acid) ergic activities. CC The nucleic acid that encodes the protein is used: (1) as primers or probes for detection/amplification, particularly for screening gene (1) receptor of expression of recombinant polypeptides; and (3) to detect allelic capnormalities in the GHBR gene (for diagnosing diseases, or expression of recombinant polypeptides; and (3) to detect allelic capnormalities in the GHBR gene (for diagnosing diseases, or susceptibility, associated with abnormal expression of GHBR): The copportion (or cells and transgenic animals expression of GHBR): The copportion of the compounds; and (3) to raise antibodies (Ab) specific for GHBR. CC the Ab are used to detect/measure (1) in diagnostic immunosassays. The agents are used to prevent or treat diseases associated with abnormal copperation of animobutyric acid) ergic and/or dopaminergia activities, e.g. caplepsy, anxiety, sleep or behavioral diseases intidated with hormone copiection of hormones (growth hormone and notolactin) that are under dopamineratic control.
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                                                                                                                                                                                        New rat brain gamma-hydroxybutyrate receptor and its encoding nucleic acid, useful for identifying agents for treating e.g. epilepsy -
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                                                                Score 449.2; DB 22; Length 1735;
Pred. No. 2.1e-98;
); Mismatches 473; Indels 133;
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2088 2326 1968 2206 TCAGGGCCGGGTGGGTTATAAAA----ATAAAGTAGGCCTTTGAGCTGTGAGCCTTTTGG CCTACTAGCGCTCTGGGGTTCGGAGTTTGGGAATTTCTCA--GAGCCAACTGGCTCAG 1005 GCTTGGGAAGGCTGGCTGCTGCTCCTCATCAGCTATGTGAAGGGGTGTGT CTGGGGCCACGTATGTTGTTAAATGGATGAAACAGGCCCTTGAGTTGGGAGCCTGCTTC CAGGIGIAGCIAAITGCICIGGIGIGGGAAIGCAG-----GCCIAAIGACAGAAAIC 2267 GCTAATGAGAAAACCTCTTAAACCCTGATAGTCAAAAGGTGTGGGGGCCATCTTTGACA AGAAATTAATTCAGAAATCAAATCTGCAGGCCAAACAAGGTGCAGGACCCAGCTTTGGCC -- TGCCTG Aregagicarccieccececereciógeciogiceas anteresas en estas en en estas en en estas en estas en estas en en estas en en estas en en estas en en estas en en estas en en estas en en estas en en estas en en 1969 GACTITAATITITICCCACTATICCTGGAGATGGGACATAGAGAGACATTGCTTTGTGCTG 1185 ACTTTGA--CTTTCCCACTGTTGCTGGAGACA------AAGACATCGTGATG AGAAATACTTGCATGATTGAGTCTGAGTCGCTAAGGGCAACTGGCCTTGAGTGACATCAA 1284 grácedreddantegdaddadaddaddateceerchdacadredeeceeranni TGGAGAAGCCAAGAAGCTAGATTTTTCATGTGAACTATCCCCGAGTTTTAAGTTGTTTGCA CCTCCCCCACCATAGGTCCCTCAGGGACAGTGCCCCCATGGGAGCCCTGGTGAGTCCACGG CTTACTAGTTCTTTGGGTTTCATGGAATTTTACAAGCTTCTAAAGGAGCAGAGTGGCTCAG -----TGTGAATCAAAGGAGGTTTGGCCTAGTGCCCAGTCTTTTAACTTAGATGCCC GGGGTGGTGGGGACTGTGGCAAACCACAGATTCCCACCTGAAATTGGTGGCTGTC--CTT Human; colon cancer; colon cancer antigen; diagnosis; detection; diadnetification; cytostatic; cardioactive; neuroprotective; vulner immunomodulatory; muscular; gynaecological; gastrointestinal; nephrotropic; antiinfective; antibacterial; gene therapy; wound; neural disorder; immune system disorder; muscular disorder; reproductive disorder; asstrointestinal disorder; reproductive disorder; actiovascular disorder; sein infectious disease; cardiovascular disorder; sein infectious disparent disorder; sein infectious disease; cardiovascular disorder; sein infectious disease; cardiovascular disorder; sein infectious disease; cardiovascular disorder; sein infectious disease; cardiovascular disorder; sein infectious disease; cardiovascular disorder; sein infectious disease; cardiovascular disorder; sein infectious disease; cardiovascular disorder; sein infectious disparent disorder; sein infectious disparent disorder; sein infectious disparent disorder; sein infectious disparent Human colon cancer antigen nucleotide sequence SEQ ID NO:205 2418 TTCAGGAATGCTGGGAACTGCTGCAGGTGGGC TTGAGGGATGCTGGGCACTGCTGCCGGGTGGC

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946
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707 TAGACTTCACCCAGGAATATTGGCAGTGCTGTGGGGCCTTTTGGAGCTGATGGAACC
                                                                                        TABATATTTACTTCAATTGCACAGATTCCAATGCAAGTCGAGAGCGATGTGGCGTTCCAT
                                                                                                                                            TCTCCTGCTGTGTCAGGGACCCTGC----GATGTCCTCAACACCCAGTGTGGCTATGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAC97991 to AAC98763 encode the human colon cancer associated proteins, called human colon cancer antigens, given in AAB53234 to AAB54006. The human colon cancer antigens can have cytostatic, candioactive, muscular; neuroprotective, immunomodulatory, gynaecological, gastrointestinal, colon be used in gene therapy. The colon cancer antigen polynuclectides, and can be used in gene therapy. The colon cancer antigen polynuclectides, proteins and antibodies to the proteins are useful for the prevention, treatment and diagnosis of colon disorders, such as colon cancer. The polynuclectides may be used in diagnostics and research, such as for chromosome identification, and as hybridisation probes. The proteins may also be used to prevent disorders such as neural disorders, immune gastrointestinal disorders, wounds, renal disorders, immune diseases, and cardiovascular disorders. AAC98764 to AAC98772 and also and cardiovascular disorders. AAC98764 to AAC98772 and also and cardiovascular disorders. ABC98764 to AAC98772 and also and an antibodia and an antibodia and an antibodia and an antibodia and an antibodia and an antibodia and an antibodia and an antibodia and an antibodia and an antibodia and an antibodia and an antibodia and antibodia and antibodia and an antibodia and an antibodia and an antibodia and an antibodia and an antibodia and an antibodia and an antibodia and an antibodia and an antibodia and an antibodia and an antibodia and an antibodia and an antibodia and an antibodia and an antibodia and an antibodia and an antibodia and an antibodia and an antibodia and an antibodia and an antibodia and an antibodia and an antibodia and an antibodia and an antibodia and an antibodia and an antibodia and an antibodia and an antibodia and an antibodia and an antibodia and an antibodia and an antibodia and an antibodia and an antibodia and an antibodia and an antibodia and an antibodia and an antibodia and an antibodia and an antibodia and an antibodia and an antibodia and an antibodia and an antibodia and an antibodia
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                                                                                                                                                                                                                                                                                                                           Colon cancer associated gene sequences, referred to as colon cancer antigens, useful for the treatment, prevention, and diagnosis of colon disorders such as colon cancer -
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Pred. No. 1.4e-96;
0; Mismatches 209; Indels
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Best Local Similarity
Matches 581; Conserv
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nucleic acid. The present sequence is useful for preventing, treating or ameliorating a medical condition and in diagnosing (susceptibility to) a pathological condition e.g. endocrine disorders e.g. Addison's disease, (cardio)vascular diseases e.g. arrhythmia and atherosclerosis, cerebrovascular diseases, neural disorders e.g. Alzheimer's and Parkinson's disease, reproductive disorders, skin disorders e.g. disorders e.g. disorders e.g. skin disorders e.g. disorders e.g. chopsis and disorders e.g. graft vs. host disease, hyperproliferative disorders e.g. neoplasms of the pancreas, ocular disorders e.g. glaucoma and infections caused by bacteria, viruses and fungi.
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                                                                                                                                                   Sequence 1174 BP; 306 A; 259 C; 291 G; 316 T; 2 other;
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                                                                                                                                                                          Score 418.6; DE
Pred. No. 4.6e-9
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ilarity 73.0%;
Conservative 0
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Gene therapy; human; 4 transmembrane superfamily receptor protein; addocrine; cardiovascular; cerebrovascular disease; neural disorder; reproductive; skin; renal system; autoimmune; hyperproliferative; ocular; bacterial infection; viral; fungal; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to isolated nucleic acids and proteins encoding human soluble 4 transmembrane superfamily receptor protein (see Accoolar-C90023 and AAB49502-B49511). The present sequence is one such nucleic acid. The present sequence is useful for preventing, treating ameliorating a medical condition and in diagnosing (susceptibility to) a pathological condition e.g. endocrine disorders e.g. Addison's disease, cerebrovascular diseases, neural disorders e.g. Alzheimer's and Parkingon's disease, reproductive disorders e.g. Alzheimer's and psoriasis, renal system disorders e.g. nephritis, (auto)immune system disorders e.g. graft vs. host disease, hyperproliferative disorders e.g. neoplasms of the pancreas, ocular disorders e.g. glaucoma and infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGCACTACAAGGGTCCTGAAGTCAGTTGTTGCATCAAATACTTCATATTTGGCTTCAATG 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated nucleic acid molecule encoding human soluble 4 transmembrane superfamily receptor protein, useful for diagnosing, treating and/or preventing disorders e.g. Alzheimer's, cancer and arrhythmia -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGCACTTCCAGGAACCCGAGGTCGGCTGCTGCGGGAAATACTTCCTGTTTGGCTTCAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              161 TCATATTTTGGTTTTTGGGAATAACATTTCTTGGAATTGGACTGTGGGCATGGAATGAAA
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Pred. No. 4.2e-87;
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es 218; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Roschke V,
                                ВР
                                                                                                                                  Clone HE8EL16 coding sequence #2.
                                  AAC90020 standard; cDNA; 1178
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99US-0137797.
99US-0138573.
99US-0149447.
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Local Similarity 71.6%;
hes 571; Conservative (
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11-JUN-1999;
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Rosen CA;
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                                                                                                        TGTTTGTAGTGGTTGGAGGCGTCATGTCCGTGGCTTTGCCGGCTGCATCGGGGCTC
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                                                                                                                                                                                   TCAATTTCTTCATTAACAACAACGTCAAGGCCTATCGGGATGACATTGACCTCCAGAACC
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The present invention relates to the isolation of novel CDNA sequences which encode human secreted proteins. The CDNA sequences have been derived from a variety of human tissues. The invention also provides method for producing proteins from these polynuclectide sequences. The proteins are useful for identifying compounds that modulate their activity and production. The sequences of the invention are useful for identifying compounds that modulate their activity and production. The sequences of the invention are useful for treating diseases such as hyperproliferative disorders (e.g. cancer), immune deficiency disorders (e.g. severe combined immunodeficiency (SCID), autoimmune disorders (e.g. multiple sclerosis), blood disorders (e.g. thrombocytopaenia), inflammatory disorders (e.g. arthritis), infectious disorders (e.g. hepatitis), allergic conditions (e.g. asthma), neurodegenerative disorders (e.g. habeimer's disease), liver fibrosis, coagulation disorders (e.g. habeimer's disease), liver fibrosis, coagulation disorders (e.g. habeimers are also useful in gene therapy, ABK15610-ABK36212 represent
                                                                                                                                                                                              Six hundred and twenty three polynucleotides derived from a variety of human tissue sources which encode secreted proteins, useful for treating immune deficiencies and disorders such as autoimmune disorders
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                                                              collins-Racie LA, Evans C;
Bowman MR, Spaulding V, Wong GG
mick RJ, Gulukota K, Graham JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA sequences of the invention that encode for novel human
                                                              Collins-Racie
                                                                                                   Resnick RJ,
                                                              Lavallie ER,
                                                                                                                                                                                                                                                                                                              Claim 1; Page 146; 393pp; English.
                                                                                     Agostino M.
Howes SH,
                       (GEMY ) GENETICS INST INC.
                                                                                   Treacy M,
Fechtel K,
                                                                 McCoy JM,
                                                                                                                                                       WPI; 2002-179322/23.
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                                            Jacobs K, P
                                                                                   Merberg D,
Clark HF,
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Sequence 1988 BP; 503 A; 434 C; 446 G; 604 T; 1 other;

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                                                                                                               TGGAATGAAAAGGAGTTCTGTCCAACATCTCTTCCATCACCGATCTCGGCGGCTTTGAC
                                                                                                                                                 CCTGTGTGGCTGTTTGTAGTGGTTGGAGGCGTCATGTCCGTGCTGCGGCTTTGCCGGCTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGTGCCCTTCTCCTGCTGTGTCAGGGACCCTGC----GATGTCCTCAACACCCAGTGT
                                            Gapa
                                          4.
   Length 1988;
Score 370; DB 24; Length 1
Pred. No. 3.2e-79;
0; Mismatches 185; Indels
14.6%;
72.4%;
                   Best Local Similarity 72.4
Matches 495; Conservative
                                                                                                                                                                                                                                                                                                                                   182
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   Query Match
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GGCTATGATGTCCGGCTCAAACTGGAGCTGGAGCAGCAGGCTCCATACACACAAAGGC 780

721

06-APR-2000; 2000US-195605P

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human genes. The genes and their corresponding secreted polypeptides are useful for preventing, treading or ameliorating medical conditions.

Useful for preventing, treading or ameliorating medical conditions.

Useful for preventing, treading or ameliorating medical conditions.

Cor by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 97 genes, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours developing products for the and circincises, blood disorders, diseases of the immune system, autoimmune diseases, inflammation, allergies, Albachimer's and cognitive disorders, atherosclerosis, diabetes, cardiovascular disorders, kidney disorders, digestive/endocrine disorders, inflections and AIDS. The sequences shown in AAY76224 to AAY76424 represent fragments of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2672 BP; 548 A; 747 C; 708 G; 661 T; 8 other;
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                                                                                                                                                                                                                                                                                     ATAGGCATTGCATTGCTGCAGATATTTGGGATATGCCTGGCCCAGAATTTGGTTAGCGAT 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; secreted protein; cancer; tumour; developmental abnormality; foetal deficiency; blood disorder; immune system disorder; inflammation; autoimmune disease; allergy; Alzheimer's disease; cognitive disorder; schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder; atherosclerosis; diabetes; cardiovascular disorder; kidney disorder; digestive disorder; endocrine disorder; infection; AlDS; leukaemia; therapy; chromosome 10; ds.
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This sequence was found to be present on human chromosome 10.
542 TGTGTGCCCCAGTTTGAGAAGTGGTTGCAGGACAATTTAACCATCGTTGCTGGTATTTTC
                                                                                                                             TGTGTGGGCCAGTTTGAGAAGTGGCTGCAGACAACCTGATCGTGGTGGCTGGGGTCTTT
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Soppet DR;
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hi Y, Young PE, Wei F, Brewer LA,
Endress GA, Ebner R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATCAAGGCAGTGAAGGCCAACTGG 924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ArceAaccrercaececeaecree 685
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Shi Y, Young PE, 1
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18-MAY-1998;
18-MAY-1998;
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18-MAY-1998;
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18-MAY-1998;
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18-MAY-1998;
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This invention relates to the cDNA sequences encoding an isolated novel human polypeptide. The protein encoded by the nucleic acid of the invention is useful for treating central and peripheral nervous system diseases (e.g. peripheral neuropathy, Huntington's disease, amyotrophic lateral sclerosis); neurodegenerative diseases (e.g. Parkinson's disease, Alzheimer's disease); autoimmune disease (e.g. Parkinson's disease, Alzheimer's disease); autoimmune disease (e.g. Systemic lupus erythematosus, rheumatoid arthritis, insulin-dependent diabetes mellitus); myeloid or lymphoid cell disorders (e.g. anaemia and thrombocytopaenia); wounds, ulcers, burns; bone disorders (e.g. catcoke, head trauma); lung or liver fibrosis; repertusion injury in various tissues; bacterial, viral or fungal infections; allergic conditions such as allergic rhinitis, asthma; coagulation disorders (e.g. haemophilia); cancer and tumours; and inflammatory diseases (e.g.
938
                                                                                                               881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; gene; 88; nervous system disorder; peripheral neuropathy; Huntington's disease; amyotrophic lateral sclerosis, haemophilia; neurodegenerative disease; Parkinson's disease; Alzheimer's disease; autoimmune disease; systemic lupus erythematosus; rheumatoid arthitis; insulin-dependent diabetes mellitus; anaemia; thrombocytopaenia; wound; ulcer; burn; bone disorder; osteoporosis; osteoarthritis; stroke; fibrosis; reperfusion nijury; infection; allergic rhinitis; asthma; coagulation disorder; cancer; tumour; inflammatory disease; septic shock; Crohn's disease; anaphylaxis; proliferation; chemotactic; differentiation; stem cell growth factor; haematopoiesis; chemotactic; haemostatic; antinflammatory; expressed sequence tag; EST.
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                                                                                                           CGTGGTGGCTGGGGTCTTTGTGGCGATCGCTCTCCTCCAGATCTTTGGTATCTGCCTGGC
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Drmanac RT;
                                                                                                                                                                                                                                                                                               939 AAGGACGCTGATCTCAGACATCGAGGCAGTGAAGGCC 975
                                                                                                                                                                                                                                                 882 CCAGAACCTTGTGAGTGACATCAAGGCAGTGAAGGCC 918
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Wang D,
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I, Wang J,
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Yang Y, Wehrman T,
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Xue AJ,
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septic shock, Crohn's disease, anaphylaxis). The protein may be used to inhibit the growth, infection or function of infectious agents such as bacteria, fungi, viruses, or to effect bodily characteristics, biorhythms or circadian cycles of rhythms. The protein may also have proliferation/differentiation, stem cell growth factor, haemactopoiesis regulation, immune stimulating or suppressing, chemokinetic, haemostatic stimulating or the invention are useful for expressing recombinant protein for analysis. The present sequence represents a novel human cDNA sequence of the invention, this sequence is an expressed sequence tag (EST) and was identified using subtractive hybridisation.
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Pred. No. 1.7e-75;
0; Mismatches 302; Indels 8;
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TGTGGCTGGCGTCTTCATCGCCATCTTGCAGATATTTGGCATCTTCCTGGCAAG 878
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Secreted protein; transmembrane protein; TANGO; human; drug screening; activity modulator; expression modulator; cancer; immunological disorder; cytostatic; immunomodulatory; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding secreted TANGO and MANGO polypeptides, useful for the prevention, diagnosis and treatment of, e.g. cancers and immune
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                                                     885 GAACCTTGTGAGTGACATCAAGGCAGTGAAGGCC
                                                                                       GACGCTGATCTCAGACATCGAGGCAGTGAAGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-138647/14.
P-PSDB; AAB87034, AAB87035, AAB87036.
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                                                                                                                                                                                                                                           ВР
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150 CCGAGGTCGGCTGCTGCGGGAATACTTCCTGTTTGGCTTCAACATTGTTTTCTGGGTGC 209

13.9%; Score 353.4; DB 22; Length 813; 67.0%; Pred. No. 2.3e-75; 0; Mismatches 251; Indels

Matches 518; Conservative

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November 21, 2003, 17:13:09; Search time 9165 Seconds (without alignments) 11328.820 Million cell updates/sec
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

jo	Homo Seque Seque Seque	equen equen enopu m Mus m omo s	AF053455 Homo sapi BC025568 Mus muscu BC026511 Mus muscu BC026574 Mus muscu AF311903 Homo sapi AX440923 Sequence BD135990 Secretory	AC019194 Homo sapi BC002920 Homo sapi AX343015 Sequence AF174603 Homo sapi AX072723 Sequence BC04424 Homo sapi AX247836 Sequence AX072711 Sequence BC024686 Mus muscu AK016798 Ciona int AF274013 Drosophil	AC124104 Nomo sapi AC123758 Mus muscu AC136719 Mus muscu AC136710 Mus muscu AC136142 Rattus no AC130985 Rattus no AC024042 Homo sapi BD07489 Secreted AC108210 Homo sapi BC001894 Drosophil AC136142 Rattus no BC003872 Mus muscu BD132536 Secreted AC136142 Rattus no BC003157 Homo sapi	ENTS p mRNA linear PRI 10-JUN-2003 ein MGC14859, mRNA (cDNA clone lete cds. Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo. Grouse, L.H., Derge, J.G.,
ID	BC010405 AX420466 BC010346 AX420468	AXO21778 AXO61778 BC041304 AF121344 AF065389 BC009704	AF053455 BC02558 BC024611 BC026574 AF311903 AX440921 AX440923	AC01934 AX343015 AX343015 AX07272 AX07272 AX072711 BC024685 AX116798	AC123758 AC123758 AC126719 AC135142 AC135142 AC135142 AC02409 BC02489 AC027699 BT004914 AC135142 BC03872 BD132536 BC03157	BC010405 BC010405 BC010405 Homo sapiens hypothetical protein MGC148 MGC:14859 IMAGE:3621871), complete cds. BC010405.1 GI:1471440 MGC. Homo sapiens (human) Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Mammalia; Butheria; Primates; Catarrhini J (bases I to 2426) Strausberg, R.L., Feingold, E.A., Grouse, L. Klausner, R.D., Collins, F.S., Wagner, L.,
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\$ Query Match	أونظوه	J-1.6044-	40,000,000	50 L 0 0 0 0 0 0 0 0 0 0	, www. www. www. www. www. www. www. ww	BC010405 Homo sapiens MGC:14859 IM BC010405.1 BC010405.1 MGC. Homo sapiens Homo sapiens Homo sapiens Ammalia; Eu 1 (bases 1 Strausner; R.D
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909 GGCCTCAGCAGAACTCTCTGACTGGGGCCCCTGGCCCAGCCCAGCCAACCAGTTT
                                           Length 2426;
                                                           Pred. No. 1.5e-205;
0; Mismatches 567;
                                               DB 9;
                                           Score 960.8;
                                           37.9%;
                                           Query Match 37.9
Best Local Similarity 69.8
Matches 1768; Conservative
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Altschul, S. F., Zeeberg, B., Buetcow, K. H., Schaefer, C. F., Bhat, N. K., Hopkins, R. F., Jordan, H., Moore, T., Max, S. I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A. A., Rubin, G. M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M. F., Casavant, T. L., Scheetz, T. E., Brownstein, M. J. Usdin, T. B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S. S., Loquellano, N. A., Peters, G. J., Abramson, R. D., Mullahy, S. J., Bosak, S. A., McEwan, P. J., McEwan, P. J., Malek, J. A., Gunaratne, P. H., Richards, S., Worley, K. C., Hale, S., Garcia, A. M., Gay, L. J., Hulyk, S. W., Villalon, D. K., Muary, D. M., Sodergren, E. J., Lu, X., Gibbs, R. A., Fahey, J., Helton, E., Ketteman, M., Yadan, A., Young, A. C., Shevchenko, Y., Boutfard, G. G., Blakesley, M. W., Touchman, J. W., Green, E. D., Dickson, M. C., Rodriguez, A. C., Grimwood, J., Schmutz, J., Myers, R. M., Butterfield, Y. S., Krzywinski, M. I., Skallska, U., Smailus, D. E., Schnerch, A., Schein, J. E., Jones, S. J. and Marra, M., Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
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PNDWALNIYFNCTDLMFSRERCGYPFSCCYRDPAEDVLINTQCGYDVRLKLELEQQGFI
HTKGCVGQFEKWLQDNLIVVAGVFMGIALLQIFGICLAQNLEQME
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This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, GenomeScan gene prediction, Similarity but not identity
                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg, R. Direct Submission Submission National Institutes of Health, Mammalian Submitted (09-JUL-2001) National Institutes Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUM-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Contact: MGC help desk
Tissue-remail.nih.gov
Tissue-remail.nih.gov
Tissue-procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
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/tissue type="Pancreas, adenocarcinoma"
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AACAAAACCTTGAAAACCACTGGCTTACGCCCACCATCTCAGAGGTTCCATGGGCCGCAG 1019 CATCAAGGCAGTGAAGGCCAACTGGATCAAACATGATGATGGCTACAAACTACTCAAATA 959 CTGGGGTGAGAAGGGCGTTCTCTCGAACATCTCAGCGCTGACAGATCTGGGGGCCTTGA GGGCAAGCACCACCACCAGGAACCCGAGGTCGGCTGCTGCGGGAAATACTTCCTGTT CGCCAAGCACCAGCATTTCCAGGAACCTGAGGTCGGCTGCTGCTGCGGGAAATACTTCCTGTT TGGCTTCAACATTGTTTTCTGGGTGCTGGAGCCCTGTTCCTGGCCATCGGCCTCTGGGC rederricaacarriererrendearecredeagecererrerregeraredecererrege CTGGGGTGAGAAGGGTGTTCTCTCCAACATCTCTGCGCTGACCGATCTGGGAGGCCCTCGA CCCTGTGTGGGTTTGTAGTGGTTGGAGGCGTCATGTCCGTGCTGGCTTTTGCCGGCTG CATCGGGGCTCTCCGGGAGACACTTTCCTGCTCAAGTTTTTCTCAGTGTTCCTTGGCCT CATTGGGGCCCTCCGGGGAGAACACCTTCCTGCTCAAGTTTTTTCTCCGTGTTCCTCGGTCT CATCTTCTTCCTGGAGCTGGCAACAGGGATCTTGGCCTTCGTATTCAAGGACTGGATTCG CATCTTCTTCCTGGAGCTGGCAACAGGGATCCTGGCCTTTGTCTTCAAGGACTGGATTCG AGACCAGCTCAATTTCTTCATTAACAACGTCAAGGCCTATCGGGATGACATTGACCT AGACCAGCTCAACCTCTTCATCAACAACGTCAAGGCCTACCGGGACGACATTGACCT CCAGAACCTCATTGACTTTGCTCAGGAATATTGGTCTTGCTGCGGAGGCCCGAGGCCTAA ccadaaccrcarridacrrrrdcrcagaaracrogrcrrrdcrgcggagccccaa TGACTGGAACCTCAATATCTATTTCAACTGCACTGACTTGAACCCGAGCCGAGAGCGCTG TGACTGGAACCTCAATATCTACTTCAACTGCACTGACTTGAACCCCAGCCGGGAGCGCTG TGGCTATGATGTCCGGCTCAAACTGGAGCTGGAGCAGCCAGGGCTCCATACACACAAAGG TGGCTACGACGTCCGGCTCAAACTGGAGCTGGAGGCAGGGCTTCATCCACCACAAAGG CTGTGTGGGCCAGTTTGAGAAGTGGCTGCAGGACAACCTGATCGTGGTGGTGGCTGGGGTCTT CTGCGTGGGCCAGTTTGAGAAGTGGCTGCAGGACAACCTGATTGTGGTGGCGGGAGTCTT 849 ATGATGACTTTGAAAACCACTGGCTTACGCCCACCATTCCGAGGTCCTGTCCACGGGGG Gaps Indels 197;

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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31.1%; Score 790.4; DB 6;
Best Local Similarity 92.3%; Pred. No. 3.7e-167;
Matches 855; Conservative 0; Mismatches 66;
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23228, a human tetraspanin family mem
Patent: WO 0216603-A 1 28-FEB-2002;
Millennium Pharmaceuticals, Inc. (US)
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Sequence 1 from Patent W00216603.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1516)
Straubberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S. I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Scheefer, C.F., Bath, P., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., Male, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Vilalon, D.K., Male, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Nadan, A., Young, A.C., Shevchenko, Y., Butterfield, Y.S., Kzzywinski, M.I., Skalski, U., Schmutz, J., Myers, R.M., Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: ogapba-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
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/ Coganisma=Mus musculus"
/ mol type="mkNa"
/ strain="C57BL/6J"
/ strain="C57BL/6J"
/ db xref="caxon:1090"
/ clone="MGC:6941 IMAGE:2811935"
/ tissue_type="Mammary tumor. WAP-TGF alpha model. 7 months
/ clone lib="NGCAP_Mam5"
/ clone lib="NGCAP_Mam5"
/ lab_host="DH10B"
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Submitted (05-JUL-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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/protein_id="AAH10346.1"
/db_xref="G1:16307593"
/db_xref="LocusID:74257"
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/db_xref="MGI:1921507"
136_..948
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/gene="2210021G21Rik"
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Mus musculus RIKEN cDNA 2210021G21 gene, mRNA (cDNA clone MGC:6941
IMAGE:2811935), complete cds.
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Catarrhini; Hominidae;
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Pred. No. 4.1e-149;
0; Mismatches 51;
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2328, a human tetraspanin family mer
2328, a human tetraspanin family mer
Patent: WO 0216603-A 3 28-FEB-2002;
Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
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                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
1333 c 235 g 19
                                                                         AX420468 813 bp
Sequence 3 from Patent W00216603
AX420468 AX420468.1 GI:21524616
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Local Similarity 93.2%;
hes 755; Conservative
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Eukaryota; Metazoa;
Mammalia; Eutheria;
  CGTGAAGGCCAACTGG
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/translation="MPGKHQPFQDPEVGCGKYPLFGFNIVFWVLGALFLAIGLWAWG
EKGYLSNISALTDLGGLDPVWLFVVVGGVMSVLGFAGCIGALRENTFLLKFFSVFLGL
IFFLELAAGTLAFVFKDWIFNNNVRATRDDLDLQNLIDFAQEYWSCCGARG
PNDWILNIYPTDLNPSRERCGVPFSCCVRDPAEDVLNTQCGYDIRLKLELEQQGSI
YKGCVGOFKWLQNNLIVVAGVLVGIALLQIFGLCLAQNLVSDIKAVKANW"
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Pred. No. 5.2e-157;
0; Mismatches 96; Indels 4;
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Pred. No. 8.5e-120;
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Losubatted (14-AUG-2000) Osamu Ohara, Kazusa DNA Research Institute,

Direct Submission

Losubatted (14-AUG-2000) Osamu Ohara, Kazusa DNA Research Institute,

Department of Human Gene Research; 1532-3, Yana, Kisarazu, Chiba
292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp,

URL:http://www.kazusa.or.jp/NEDO, Tel:81-438-52-3913,

Fax:81-438-52-3914)

NEDO human CDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; CDNA full insert
sequencing: Research Association for Biotechnology; CDNA library

Construction, 5'- & 3'-end one pass sequencing and clone selection:

Kazusa DNA Research Institute.
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ONLVSDIKAVKANWSKWNDDFENHWLTPTISEVLSTAGPQQNSLTGAPPSRHVF
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                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo. I (bases I to 4445)
Ohara, O., Nagase, T., Kikuno, R. and Okumura, K.
The nucleotide sequence of a long cDNA clone isolated from human
                                                     AAAGGCTGTGTGGGCCAGTTTGAGAAGTGGCTGCAGGACAACCTGATCGTGGTGGCTGGG
                                                                            GTCTTTGTGGGCATCGCTCTCCAGATCTTTGGTATCTGCCTGGCCCAGAACCTTGTG
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AK024427 4445 bp mRNA linear Homo sapiens mRNA for FLJ00016 protein, partial cds. AK024427
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/db_xref="taxon:9606"
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Published Only in DataBase (2000)
2 (bases 1 to 4445)
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          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCAGTITGAGAAGIGGCIGCAGGACAACCIGAICGIGGIGGCIGGGGTCITIGIGGGCAI 848
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eucoleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                              133 CCAGCACTTCCAGGAACCCGAGGTCGGCTGCTGCGGGAAATACTTCCTGTTTGGCTTCAA
                                                                                                                                        CATTGTTTTCTGGGTGCTGGGGGCCCTGTTCCTGGCCATCGGCCTCTGGGCCTGAGGTGA
                                                                                                                                                                                                                            TGTCATCTTCTGGCTCTTGGGGTTTCTTGGAGTTGGTCTGGGCGTTGGGGGTGA
                                                                                                                                                                                                                                                                                   GAAGGGTGTTCTCTCCCAACATCTCTGCGCTGACCGATCTGGGAGGCCTCGACCCTGTGTG
                                                                                                                                                                                                                                                                                                       248 AAAGGTGTGCTTTCCAACATTTCCTCTATCACAGATCTTGGGGGTTTTGATCCAGTGTG
                                                                                                                                                                                                                                                                                                                                                                   GCTGTTTGTAGTGGTTGGAGGCGTCATGTCCGTGCTGGGCTTTGCCGGCTGCATCGGGGC
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Mus musculus tetraspanin Tspan-5 (Tspan5) mRNA, complete cds
                            Score 465.2; DB 5; Length
Pred. No. 7.1e-94;
0; Mismatches 213; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           908 CGTCCGAGCCAGCTGGAATTATTATCCTGGATACAAGTGC 951
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                            Query Match
Best Local Similarity 73.7%;
Matches 607; Conservative
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/brotein id="AAH41304.]

/brotein id="AAH41304.]

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YKGPEVSCCIKKFIFFORVIFFULGLFPLGVCHWAWSEKGVLSNISSITDLGGFDPWM
YKGPEVSCCIKKFIFFORVIFFULGLFPLGVCHAWSEKGVLSNISSITDLGGFDPWM
OLQFFINNNIRAYRDDIDLQNLDFTPLGYPCGAFGADDWMINIYFRCTDSMASRER
GGVPFSCCTKDPABDVINTQCSYDVRQKFELDQFTIHTKGCVPQFEKWLQDNLTIVA
GVFIJALLQIFGICLAQNLVSDIEAVRASW"
                                                                                                                                                                                                                                                                                              BC041304 11685 bp mRNA linear VRT 14-JAN-2003 Xenopus laevis, Similar to transmembrane 4 superfamily member 9, clone IMAGE:4683897, mRNA, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           be found
                                                                      667
Eukaryota; Metazoa; Chordata; Craniata; Verrebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus.
1 (bases 1 to 1685)
Klein, S. and Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clone distribution: MGC clone distribution information can be fou through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 94 Row: g Column: 18
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (16-DEC-2002) National Institutes of Health, Xenopus (Collection (XGC), National Institute of Child Health and Human Development, 6100 Executive Boulevard, Room 4801, Rockville, MD 20892-7510, USA
                                                                AACCTCAATATC - TATTTCAACTGCACTT-GAACCCGAGCCGAGAGCGCTGCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgabbs remail.nih.gov
Tissue Procurement: Dr. Igor Dawid
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
http://www.systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anurad
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="Similar to transmembrane 4 superfamily
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                                                                                                                                                                         GIGCCCTTCTTCTGCTGGGTAAGGACCCTGCGGAAGACGTC 728
                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopus laevis (African clawed frog)
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                                                                                                                                                                                                                                                                                                                                                                                  BC041304.1 GI:27735442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC Project
Contact: XGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  456
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                                                                                                                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
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AUTHORS
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JOURNAL
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01-FEB-2000

997 790 850

910

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A48...1154
/note="similar to Tspan-5; TM4SF"
/codon_start=!
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                                                                                                                                                                                                                                                           PRI 28-APR-2000
                                                                                                                                                                                                                                                                                                                                                                            Submitted (14-MAY-1998) INSERM U268, 14 av Paul Vaillant Couturier, Villejuif 94807, France
Location/Qualifiers
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1 (bases 1 to 1405)
Serru, V., Dessen, P., Boucheix, C. and Rubinstein, E.
Sequence and expression of seven new tetraspans
Biochim. Blophys. Acta 1478 (1), 159-163 (2000)
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      TITCCTGCTGCACTAAAGACCCCGCGGAAGATGTCATCAACACTCAGTGTGGCTATGATG
                                                                                                 TCCGGCTCAAACTGGAGCTGGAGCAGCAGGCTCCATACACACCAAAGGCTGTGTGGGGCC
                                                                                                                                                             ccaddcadaaaccadaagingaccaacagarngraarcracacaaaaggcrgrgrgcccc
                                                                                                                                                                                                                         791 AGTITGAGAAGTGGCTGCAGGACAACCTGATCGTGGTGGCTGGGGTCTTTGTGGGCATCG
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Pred. No. 1.5e-88;
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Rubinstein,E., Serru,V. and Boucheix,C.
Direct Submission
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Homo sapiens tetraspan NET-4 mRNA,
AF065389
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/organism="Homo sapiens"
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/db & Xref="taxon:9606"
/clone="IMAGE ID 219547"
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      Garcia-Frigola, C., de Lecea, L. and Soriano, E.
Mouse Tapan-5 CDNA cloning
Uppublished
2 (bases 1 to 3175)
Garcia-Frigola, C., de Lecea, L. and Soriano, E.
Direct Submission
Submitted (20-JAN-1999) Dept. of Animal and Plant Cell Biology,
University of Barcelona, Av. Diagonal 645, Barcelona 08028, Spain
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477

found

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KGCVPQFEKWLQDNLTIVAGIFIGTALLQIFGICLAQNLVSDIEAVRASW"
25 a 354 c 385 g 352 t
                                                         Genome
CA 94305
                                                                                                                                                                                                                                     Clone distribution: MGC clone distribution information can be found through the 1.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 14 Row: h Column: 4
This clone was selected for full length sequencing because it passed the following selected for full length sequencing by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGGAGCTGGCAACAGGGATCTTGGCCTTCGTATTCAAGGACTGGATTCGAGACCAGCTCA 494
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 943
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGCACTTCCAGGAACCCGAGGTCGGCTGCTGCGGGAAATACTTCCTGTTTGGCTTCAACA
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Pred. No. 1.5e-88;
0; Mismatches 209; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue type="Pancreas, epithelioid
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                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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Best Local Similarity 73.2
Matches 581; Conservative
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Homo sapiens, tetraspan 5, clone MGC:9300 IMAGE:3895933, mRNA,
complete cds.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1416)
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Submitted (19-JUN-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAGACTICACCCAGGAATATIGGCAGIGCIGIGGGCTTTIGGAGCTGATGATGAAGCC
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                                                         TGGAGCTCACTGCCGGAGTTCTAGCATTTGTTTTCAAAGACTGGATCAAAGACCAGCTGT
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                              AGGGTGTTCTCTCCAACATCTCTGCGCTGACCGATCTGGGAGGCCTCGACCCTGTGTGGC
                                                                                                                                 TGTTTGTAGTGGTTGGAGGCGTCATGTCCGTGCTGGGCTTTGCCGGCTGCATCGGGGCTC
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Contact: MGC help desk
Email: cgapbs-rømail.nih.gov
Tissue Procurement: ATCC
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BC025568 2428 bp mRNA linear ROD 16-APR-2003
Mus musculus DNA segment, Chr 14, ERATO Doi 226, expressed, mRNA
(CDNA clone MGC:36595 IMAGE:5322531), complete cds.
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Sciurognathi; Muridae; Murinae; Mus.
                                                          362 AGCACTACAAGGGTCCTGAAGTCAGTTGTTGCATCAATACTTCATATTTGGCTTCAATG
                                                                                                                                                      AGGGTGTTCTCCAACATCTCTGCGCTGACCGATCTGGGAGCCTCGACCTGTGGC
                                                                                                                                                                          AAGGAGTTCTGTCCAACATCTCTTCCATCACCGATCTCGGCGGGCTTTGACCCAGTTTGGC
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                                                                                            TTGTTTTTCTGGGTGCTGGAGCCCTGTTCCTGGCCATCGGCCTCTGGGCCTGGGGGTGAGA
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Mui
1 (bases 1 to 2428)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
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Mismatches
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/product="tetraspan TM4SF"
/brotein_id="AAG69712.1"
/db_xref="di-295865"
/translation="MSGKHYKGPEVSCCIKYFIFGFNVIFWFLGITFLGIGLWAWNEK
/translation="MSGKPYKGPEVSCCIKYFIFGFNVIFWFLGITFLGIGLWAWNEK
/translation="MSGKPYKGPEVSCCIKYFIFGFNVIFWFLGYFLGITFFLEL
/translation="MSGKPYKGPFNNVIFWFLUVGGYDAGCIGALRENTFLSVFLGITFFLEL
TAGVLAFVFKDWIKDGINFFINNNIFWRARDDININTQGGYDARQKPEVDQQIVIYTKGCV
PQFEKWLQDNLITIVAGIFIGIALLQIFGICLAQNLVSDIEAVRASW"
354 c 384 g 345 t 16 others
                                                                                                                                                                                                                                                                                                                                                                                                                                              AF053455 1408 bp DNA linear PRI 03-NOV-1998
Homo sapiens tetraspan TM4SF (TSPAN-5) gene, complete cds.
AF053455
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                          824 TANATATTTACTTCANTTGCACAGATTCCANTGCAAGTCGAGAGCGATGTGGCGTTCCAT
                                                                        TCTCCTGCTGTGTCAGGGACCCTGC - - - GATGTCCTCAACACCCCAGTGTGGCTATGATG
                                                                                                                                       731 TCCGGCTCAAACTGGAGCTGGAGCAGCAGGGCTCCATACACACAAAGGCTGTGTGGGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Todd.S.C., Doctor.V.S. and Levy,S.

Todd.S.C., Doctor.V.S. and Levy,S.

Direct Submission
Submitted (12-MR-1998) Medicine, Stanford, 300 Pasteur
Stanford, CA 94305, USA
Location/Qualifiers
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Todd,S.C., Doctorry,S. and Levy,S.
Todds,C.C., Doctorry, S. and Levy,S.
tetraspanin/TM4SF family
Biochim. Biophys. Acta 1399 (1), 101-104 (1998)
9714763
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Pred. No. 3e-81;
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
352. .1146
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/gene="TSPAN-5"
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71.8%;
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max., S.I., Wang, J., Haieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Worley, K.C., Malek, J.A., Gunaratne, P.H., Richards, S., Vilalon, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiling, W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length brown with many and mouse cDNA sequences
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Contact: MGC help desk

Tissue Procurement: Jeffrey Green M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Parayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: National Institutes of Health Intramural

Sequencing Center (NISC)

Gaithersburg, Maryland;

Web site: http://www.nisc.nih.gov/

Contact: nisc mgc@nhgri.nih.gov

Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,

Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C.,

Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C.,

Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,

Maduco,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,

McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,

Tsurgeon,C., Voget,J.L., Malker,M.A., Wetherby,K.D., Wiggins,L.,

Young,A., Zhang,L.H. and Green,E.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (06-MAR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov/Series: IRAK Plate: 56 Row: j Column: 21 This clone was selected for full length sequencing because it passed the following selection criteria: GenomeScan gene prediction.
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64. .876

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    /strain="FVB/N"

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| FLELAVAVLAFLFQDWVRDRFREFFESNIKSYRDDIDLQNLIDSLQKANQCGAYGPE
| DWDLNYFNICSGASYSREKCGYPFSCCVPDPAQKVVWTGCGYDVRIQLKSKWNEFIFT
| KGCIQALEGWLPRNIYIVAGVFIAISLLQIFGIFLARTLISDIEAVKAGHHF"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     559 GICTACTICAACTGCAGTGGTGCCAGCTACAGCCGAGAAATGTGGGGGTACCCTTCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGCTGTGTGTCAGGGACCCTGC----GATGTCCTCAACACCCCAGTGTGGCTATGATGTCCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTCAAACTGGAGCTGGAGCAGGGCTCCATACACACCAAAGGCTGTGTGGGGCCAGTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITIGCTCAGGAATATTGGTCTTGCTGCGGAGGCCCTAATGACTGGAACCTCAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.5%; Score 368.8; DB 10; Length
llarity 67.9%; Pred. No. 3.7e-72;
Conservative 0; Mismatches 247; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      624 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140 TTCCAGGAACCCGAGGTCGCTGCTGCGGGAATACTTCCTGTTTGGCTTCAACATTGTT 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAGAACACTITCCTGCTCAAGITITTCTCAGTGTICCTTGGCCTCATCTTCTTCCTGGAG 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  310 GAGAACATCTGCCTGCTCAAGTTTTTCTGTGGGGCCATTGTGCTCATCTTCTTCCTGGAA 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               250 TIGATGGIGGGCGIGGIGAIGITCACACIGGGATICGCAGGCTGIGGGGGCCCTLCGA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               croscos es de contrator de contrator de la contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de contrator de c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           550 GTCTACTTCAACTGCAGTGCCAGCTACAGCCGAGAGAAATGTGGGGTACCCTTCTCC 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGCTGTGTCAGGGACCCTGC----GATGTCCTCAACACCCCAGTGTGGCTATGATGTCCGG 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTCAAACTGGAGCTGGAGCAGGGCTCCATACACACCAAAGGCTGTGTGGGCCAGTTT 795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    190 GTGCTGTCCGACCTCACCAAGGTGACCCGGTTGCATGGAATCGACCCCGTCGTGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70 racrcdaacecceaedreaeriecreeracaagracerecrecricaecracaararareere
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTAGTGGTTGGAGGCGTCATGTCCGTGCTGGCTTTTGCCGGCTGCATCGGGGCTCTCCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           620 ATCTATITICAACTGCACTGACTTGAACCCGAGCCGAGAGCGCTGCGGGGTGCCCTTCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTCTGGGTGCTGGGAGCCCTGTTCCTGGCCATCGGCCTTGGGCCTGGGGAAGGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              670 ATTCAGCTGAAGAGCAAGTGGGATGAGTTCATCTTTACAAAAGGATGCATCCAGGCTCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 14.5%; Score 368.8; DB 10; Length 2498; Best Local Similarity 67.9%; Pred. No. 3.7e-72; Matches 531; Conservative 0; Mismatches 247; Indels 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       681 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Colling, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
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Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquallano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whilting, M., Madan, A., Kodrigues, S.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Onnes, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
                                                                                                     ROD 16-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         be found
                                                                                                                                                                                                                                                                                                                                         Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Dases 1 to 2498)
1 (Dases 1 to 2498)
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Submitted (01-MAR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                             SCO24611 . 2498 bp mRNA linear ROD 16-APR-21
4us musculus DNA segment, Chr 14, ERATO Doi 226, expressed, mRNA
(cDNA clone MGC:28503 IMAGE:4188261), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 37 Row: e Column: 12 This clone was selected for full length sequencing because it passed the following selection criteria: GenomeScan gene prediction, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:10090"
/clone="MGC:28503 IMAGE:4188261"
/tissue_type="Salivary gland, 10 week old female mouse"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs.r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing Upy: Baylor College of Medicine Human Genome
Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
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                                                                                      2498 bp
                                                                                                                                                                                                                                                                                                           Mus musculus (house mouse)
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/strain="FVB/N"
                                                                                                                                                                                                                                        BC024611.1 GI:19354053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 2498)
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                                                                                         LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
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TITLE
JOURNAL
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MEDLINE
PUBMED
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AUTHORS
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COMMENT
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499

559

549

619

699

855 789

ACCESSION VERSION KEYWORDS SOURCE

REFERENCE AUTHORS

RESULT 14

g ò 8

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BC026574

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/#stain="rybB/N"
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DWDLWYFROSGASYSREKCGVFFSCCVPDPAQKVVNTQCGYDVRIQLKSKWDEFIFT
KGCIQALEGWLPRNIVAQVFIAISLLQIFGIFLARTLISDIEAVKAGHHF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  199
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0; Mismatches 247; Indels
                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
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                                                                                                                                                                                                                                                  1. .2500
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/note="synonym: MG036554"
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50. .862
                                                                                                                                                                                                                            /note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 368.8;
organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.5%;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mans musculus

Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 2500)

Strausberg, E.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Magner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.J., Wang, J., Hsieh, F.,
Diatchenko, L., Maruslana, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Bouffard, G.G., Blakesley, R.W., Touchman, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchen, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalaka, U., Sanilus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences

V. 2188257
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Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Parayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Library Parayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site:
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Blickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
                                                                                                                                                                                                                                                     BCO26574 2500 bp mRNA linear ROD 16-APR-2003 Mus musculus DNA segment, Chr 14, ERATO Doi 226, expressed, mRNA (CDNA clone MGC:36554 IMAGE:4954874), complete cds.
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Submitted (02-APR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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This clone was selected for full length sequencing because it passed the following selection criteria: GenomeScan gene prediction.
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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Mus musculus
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GVLSDLTKVTRMHGIDPVVLVLMVGVVMFTLGFAGCVGALRENICLLNFFCGTIVLIF
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KGCIQALESWLPRYTVAGVFIAISLLQIFGIFLARTLISDIBAVKAGHHF"
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                                                ATTCAGCTGAAGAGCAAGTGGGATGAGTTCATCTTTACAAAAGGATGCATCCAGGCTCTG 724
                                                                                                GAGAAGTGGCTGCAGGACAACCTGATCGTGGTGGCTGTTTTGTGGGCATCGCTCTC 855
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Direct Submission
Submitted (06-007-2000) Department of Immunology, Second Military
Medical University & Shanghai Brilliance Biotechnology Institute,
800 Xiangyin Rd., Shanghai 200433, P.R.China
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2553)
Zhang, W., Li,N., Wan,T. and Cao,X.
Identification of novel membrane proteins
Unpublished
2 (bases 1 to 2553)
CTCAAACTGGAGCTGGAGCAGGCTCCATACACACCAAAGGCTGTGTGGGCCAGTTT
                                                                                                                                                                                             CCGAGGTCGCTGCTGCGGGAAATACTTCCTGTTTGGCTTCAACATTGTTTTCTGGCTGC
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Homo sapiens DC-TM4F2 precursor, mRNA, complete cds.
AF311903.1 GI:22266721
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larity 67.0%; Pred. No. 1.1e-68;
Conservative 0; Mismatches 251;
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/codon_start=1
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/protein_id="AAM94899.1"
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/organism="Homo sapiens"
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                      TCCTGCTCAAGTTTTTCTCAGTGTTCCTTGGCCTCATCTTCTTCCTGGAGCTGGCAACAG
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e : 9172 secs
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